SEQUENCE' LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

Goodearl, Andrew Stroobant, Paul Minghetti, Luisa ₩aterfield, Michael Marchionni, Mark dhen, Mario Hiles, Ian

(ii) TITLE OF INVENTION:

GLIAL MITOGENIC FACTORS, THEIR PREPARATION AND USE

(iii) NUMBER OF SEQUENCES:

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:

(B) STREET:

(C) CITY:

(D) STATE: (E) COUNTRY:

(F) ZIP:

Clark & Elbing LLP 17d Federal Street

Boston

189

Massachusetts, U.S.A. 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:

(B) COMPUTER: (C) OPERATING SYSTEM:

Windows95

3.5" D+Oskette, 1.44 Mb IBM Compatible Pentium

(D) SOFTWARE:

FastSeq Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

08/736 019

(B) FILING DATE:

22-OCT 1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/471,833

(B) FILING DATE:

06-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/036,555

(B) FILING DATE:

24-MAR-199B

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/965,173

(B) FILING DATE:

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(A) APPLICATION NUMBER: 07/907,138

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(A) APPLICATION NUMBER: 07/940,389

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			APPLICATION NUMBER: FILING DATE:	07/863,703 03-APR-1992
	(vii)	PRI	OR APPLICATION DATA	
			APPLICATION NUMBER:	UK 91 07566.3 10-APR-1991
	(viii	i) A	TTORNEY/AGENT INFORMA	ATION:
		(B)	NAME: REGISTRATION NUMBER: REFERENCE/DOCKET NUM	
	(ix)	TELE	COMMUNICATION INFORM	AFION:
		(B)	TELEPHONE: TELEFAX: TELEX:	(617) 428-0200 (617) 428-7045
(2)I	NFORM	ITA	ON FOR SEQUENCE IDENT	CIFICATION NUMBER: 1:
	(i) S	SEQUE	ENCE CHARACTERISTICS:	
		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	8 amino acid
	(xi)	SEQU	JENCE DESCRIPTION: SE	10 NO: 1:
Phe 1	Lys C	Sly P	Asp Ala His Thr Glu 5	
(2)	INFOR	TAMS	ON FOR SEQUENCE IDEN	TIFICATION NUMBER: 2:
	(i) S	EQUE	ENCE CHARACTERISTICS:	
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	13 amino acid linear
	(ix)	FEA	ATURE:	
Argi	nine;	(D) : Xaa	OTHER INFORMATION: a in position 12 is a	Xaa in position 1 is Lysine or unknown.
	(xi)	SEQU	JENCE DESCRIPTION: SE	EQ ID NO: 2:
Xaa	Ala S	Ser I	eu Ala Asp Glu Tyr (Glu Tyr Met Xaa Lys
1			5	10
(2)	INFOF	RMAT]	ON FOR SEQUENCE IDEN	TIFICATION NUMBER: 3:
	(i) S	EQUE	ENCE CHARACTERISTICS:	
		(B)	LENGTH: TYPE: STRANDEDNESS:	12 amino acid

	(D) TOPOLOGY:	linear	
	(ix) FEATURE:		
Argi	(D) OTHER INFORMATION: nine; Xaa in position 10 is u	Xaa in position 1 is	Lysine or
	(xi) SEQUENCE DESCRIPTION: SEC	Q ID NO 3:	
Xaa 1	Thr Glu Thr Ser Ser Ser Gly Le 5	eu Xaa Ieu Lys 10	
(2)	INFORMATION FOR SEQUENCE IDENT	TIFICATION NUMBER:	4:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	9 amino acid linear	
	(ix) FEATURE:		
	(D) OTHER INFORMATION:	Xaa in position 1 is	Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SEC	Q ID NO: 4:	
Xaa 1	Lys Leu Gly Glu Met Trp Ala G 5	lu	
(2)	INFORMATION FOR SEQUENCE IDENT	rification number:	5:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	amino acid limear	
	(ix) FEATURE:		
	(D) OTHER INFORMATION:	Xaa in position 1 is	Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SEG	Q ID NO: 5:	
Xaa 1	Leu Gly Glu Lys Arg Ala 5		
(2)	INFORMATION FOR SEQUENCE IDENT	rification number:	6:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	16 amino acid linear	
	(ix) FEATURE:		
	(D) OTHER INFORMATION:	Xaa in position 1 is	Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SEC	Q ID NO: 6:	

>

Xaa	aa Ile Lys Ser Glu His Ala Gly Leu Ser	Ile Gly Asp	Thr Ala Lys
1	1 5 10		15
(2)	2) INFORMATION FOR SEQUENCE IDENTIFICA	TION NUMBER:	7:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 13 (B) TYPE: amino (C) STRANDEDNESS: (D) TOPOLOGY: linea	1	
	(ix) FEATURE:		
	(D) OTHER INFORMATION: Xaa i	n position 1	is Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SEQ ID N	o ∫ 7:	
Xaa	a Ala Ser Leu Ala Asp Glu Tyr Glu Tyr	Met Arg Lys	
1	1 5 10		
(2)) INFORMATION FOR SEQUENCE IDENTIFICA	TION NUMBER:	8:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: amino (C) STRANDEDNESS: (D) TOPOLOGY: linea (ix) FEATURE:		
	(D) OTHER INFORMATION: Xaa i	n position 1	is Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SEQ ID N	Ð: 8:	
Xaa 1	a Ile Lys Gly Glu His Pro Gly Leu Ser 1 5 10	Ile Gly Asp	Val Ala Lys 15
(2)) INFORMATION FOR SEQUENCE IDENTIFICA	TION NUMBER:	9:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 13 amino linea		
	(ix) FEATURE:		da toda e
Argi	(D) OTHER INFORMATION: Xaa i ginine and Xaa in position 12 is unkno	own.	is Lysine or
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	O: 9:	
Xaa	a Met Ser Glu Tyr Ala Phe Phe Val Gln	Thr Xaa Arg	
1	1 5 10		

(0)			- /
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	10:
	(i) SEQUENCE CHARACTERISTICS:	,	
	(A) LENGTH: (B) TYPE:	14 amino acid	•
	(C) STRANDEDNESS: (D) TOPOLOGY:	linear	
	(ix) FEATURE:		
		You in position 1 is	Turka an Barkala
		Xaa in position 1 is	Lysine or Arginine.
	(xi) SEQUENCE DESCRIPTION: SE	/	
Xaa	Ser Glu His Pro Gly Leu Ser I		S
1	5	10	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	11:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE:	10/ amino acid	
	(C) STRANDEDNESS: (D) TOPOLOGY:	linear	
	, ,		
	(ix) FEATURE:		T
Arg	(D) OTHER INFORMATION inine; Xaa in position 8 is unl	Xaa in position 1 is known.	Lysine or
	(xi) SEQUENCE DESCRIPTION SEC	Q ID NO: 11:	
Xaa	Ala Gly Tyr Phe Ala Glu Xaa A	la Arg	
1	5	10	
	X		,
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER:	12:
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: (B) TYPE:	9 amino acid	
	(C) STRANDEDNESS: (D) TOPOLOGY:	linear	
	(ix) FEATURE:		
		Xaa in position 1 is	Lysine or
Arg:	inine; Xaa in position 7 is unl	known.	Lysine of
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 12:	
Xaa 1	Lys Leu Glu Phe Leu Xaa Ala L	ys	
1			
(2)	INFORMATION FOR SEQUENCE IDENT	TIFICATION NUMBER:	13:
	(i) SEQUENCE CHARACTERISTICS:		
	•		

		(B)	LENGTH: TYPE: STRANDEDNESS:	11 amino acid		
			TOPOLOGY:	linear		
	(ix)	FEAT	TURE:	/		
		(D)	OTHER INFORMATION:	Xaa in position 1 is	Lysine	or Arginine.
	(xi)	SEO	JENCE DESCRIPTION: SE	O TD NO: 13:		
Xaa			Glu Met Ala Ser Glu G	/		
1			5	10		
(2)	INFOR	TAM	ON FOR SEQUENCE IDEN	TIFICATION NUMBER:	14:	
	(i) S	EQUE	ENCE CHARACTERISTICS:			
			LENGTH: TYPE:	10 amino/acid		
		(C)	STRANDEDNESS: TOPOLOGY:	linear		v
	(ix)			X		
	(IX)			Van in position 1 is	Treatmo	om Americaine
	, , ,	(D)	OTHER INFORMATION	_	пувтне	or arginine.
			JENCE DESCRIPTION: SE			
Xaa	Ala L	ys G	Glu Ala Leu Ala Ala L	eu Lys		
1			5	10		
(2)	INFOR	ITAM	on for sequence iden	TIFICATION NUMBER:	15:	
	(i) S	EQUE	ENCE CHARACTERISTICS:			
			LENGTH: TYPE:	8 amino acid		
		(c)	STRANDEDNESS:	linear		
			TOPOLOGY:/	Illear		
	(ix)		/			
		(D)	/	Xaa in position 1 is	Lysine	or Arginine.
	(xi)	SEQU	JENCE DESCRIPTION: SE	Q ID NO: 15:		
Xaa 1	Phe V	al I	Leu 🕅 Ala Lys Lys 5			
(2)	INFOR	RMATI	ON FOR SEQUENCE IDEN	TIFICATION NUMBER:	16:	
	(i) S	EQU	/ ENCE CHARACTERISTICS:			
		(A)	LENGTH:	6		
		(B/) (C)	TYPE: STRANDEDNESS:	amino acid		
		(Δ)		linear		

	(ix) FEATURE:	
	(D) OTHER INFORMATION: X	aa in position 1 is Lysine or Arginine
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 16:
Xaa 1	Leu Gly Glu Met Trp 5	
(2)	INFORMATION FOR SEQUENCE IDENTI	FICATION NUMBER: 17:
	(i) SEQUENCE CHARACTERISTICS:	
	(B) TYPE: a (C) STRANDEDNESS:	6 mino acid inear
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 17:/
Glu 1	. Tyr Lys Cys Leu Lys Phe Lys Trp 5	Phe Lys Lys Ala Thr Val Met 10 15
(2)	INFORMATION FOR SEQUENCE IDENTI	FICATION NUMBER: 18:
	(i) SEQUENCE CHARACTERISTICS:	1
	(C) STRANDEDNESS: /	mino acid inear
	(ix) FEATURE: (D) OTHER INFORMATION: X	aa in position 8 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 18:
Glu 1	Ala Lys Tyr Phe Ser Lys Xaa Asp	Ala 10
(2)	INFORMATION FOR SEQUENCE IDENTI	FICATION NUMBER: 19:
	(i) SEQUENCE CHARACTERISTICS:	
	(C) STRANDEDNESS:	mino acid inear
	(ix) FEATURE:	
		aa in position 2 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ	
Glu 1	Xaa Lys Phe Tyr Val Pro 5	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
Asp Pro Met Val Ser Phe Pro Val Ala Leu 20 25
(2) INFORMATION FOR SEQUENCE IDENTIFICATION/NUMBER: 21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2003 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ix) FEATURE:
(D) OTHER INFORMATION: N in positions 31 and 32 could be either A or G.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
GGAATTCCTT TTTTTTTTT TTTTTTTTT NNTTTTTTT TGCCCTTATA CCTCTTCGCC 60
TTTCTGTGGT TCCATCCACT TCTTCCCCT CCTCCCCA TAAACAACTC TCCTACCCCT 120
GCACCCCCAA TAAATAAATA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGTGCTG 180
CGAGGGGAAG GAAAAGGGAG GCAGCGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC 240
AGAAGCCCGC ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC CGC Met Arg Trp Arg Arg Ala Pro Arg Arg 1
TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg 10 15 20 25
TCG TCG CCG CCG CTG CCG CTG CCA CTA CTG CTG CTG GGG ACC Ser Ser Pro Pro Leu Pro Leu Leu Leu Leu Leu Gly Thr 30 35 40
GCG GCC CTG CCG GGG GCG GCC GCC AAC GAG GCG GCT CCC GCG Ala Ala Leu Ala Pro Gly Ala Ala Ala Gly Asn Glu Ala Ala Pro Ala 45 50 55
GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG Gly Ala ser Val Cys Tyr Ser Ser Pro Pro Ser Val Gly Ser Val Gln 60 65 70
GAG CTA GCT CAG CGC GCC GCG GTG GTC ATC GAG GGA AAG GTG CAC CCG 531

Glu	Leu 75	Ala	Gln	Arg	Ala	Ala 80	Val	Val	Ile	Glu	Gly 85	Lys	Val	His	Pro	/	
CAG Gln 90	CGG Arg	CGG Arg	CAG Gln	CAG Gln	GGG Gly 95	GCA Ala	CTC Leu	GAC Asp	AGG Arg	AAG Lys 100	GCG Ala	GCG Ala	GCG Ala	GCG Ala	GCG/ Al⁄a 1⁄05	/	579
					TGG Trp												627
					CCG Pro												675
					TGG Trp												723
					CCC Pro												771
					TTG Leu 175												819
GGG Gly	ACC Thr	TGG Trp	GGC Gly	CAC His 190	CCC Pro	GCC Ala	TTC Phe	CCC Pro	fcc Ser 195	TGC Cys	GGG Gly	AGG Arg	CTC Leu	AAG Lys 200	GAG Glu		867
GAC Asp	AGC Ser	AGG Arg	TAC Tyr 205	ATC Ile	TTC Phe	TTC Phe	ATG Met	GAG Glu 210	CCC Pro	GAC Asp	GCC Ala	AAC Asn	AGC Ser 215	ACC Thr	AGC Ser		915
					TTC Phe												963
					GAG Glu	,											1011
					AAA Lys 255												1059
					CGG Arg												1107
					AAG Lys												1155
					ATA Ile												1203
ATT Ile	AAC/ Asn 21/5	/ AAA	GCA Ala	TCA Ser	CTG Leu	GCT Ala 220	GAT	TCT Ser	GGA Gly	GAG Glu	TAT Tyr 225	ATG	TGC Cys	AAA Lys	GTG Val		1251

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val 230 245	1299/
GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val 250 255	1/347
AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys 265 270 275	1395
TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAC TGC Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys 280 285 290	1443
CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser 295	1491
TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT CAA Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu 400 405 410	1530
TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCTCA GATTCCACCT	1590
AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA	1650
TTAACAAAAG CAATTGTATT ACTTCCTCTG TZCGCGACTA GTTGGCTCTG AGATACTAAT	1710
AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT	1770
AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA	1830
TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA	1890
AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT	1950
CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA	2003

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH (B) TYPE:

12

amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

linear

(ix) FEATURE:

- OTHER INFORMATION: Xaa in position 11 is unknown.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
1 10

(2)	INFO	RMAT:	ION FOR	SEQUENCE	IDENT	IFICATION NUMBER:	23:
	(i)	SEQUI	ENCE CHA	ARACTERIST	rics:		
		·/	LENGTH:			11 amino acid	
		(C)	TYPE:				,
	,, ,	,	TOPOLOG	iΥ:	•	linear	
	(ix)		FURE:				, ,/
		, ,				Xaa in position 9	is unknown.
						ID NO: 23:	
Thr	Glu	Thr :	Ser Ser	Ser Gly I	Leu Xaa	,	
1			5			10	,
(2)	INFO	RMAT	ION FOR	SEQUENCE	IDENT	IFICATION NUMBER:	24:
	(i)	SEQU	ENCE CHA	ARACTERIST	rics:		
			LENGTH:	:		12 amino avid	
		(C)	STRANDE			linear	
		(D)	TOPOLOG	31:	•	illiear	
	(!)	a=0	TENTAL DE	aco tomico		Z 70 24	
						ID NO: 24:	
	ser	Leu A	_	Giu Tyr (31u 17y	r Met Arg Lys	
1			5			10	
(2)	INFO	RMAT	ION FOR	SEQUENCE	IDENT:	IFICATION NUMBER:	25:
	(i)	SEQU	ENCE CHA	ARACTERIST	rics:		
			LENGTH:	: /	:	9 amino acid	
		(C)	STRANDE			linear	
	()		/	5/L :	•	IIIIeai	
	(1X)		TURE:	T17000W100		erio di constituti de	
		(D)				Xaa in position 7	is unknown.
						ID NO: 25:	
Ala 1	Gly	Tyr	Phe Ala 5	Glu Xaa A	Ala Ar	g	
(2)	INFO	RMAT:	ION FOR	SEQUENCE	IDENT	IFICATION NUMBER:	26:
	(i)/	/ SEQU	ENCE CHA	ARACTERIST	rics:		
			LENGTH:	:		10	
		(B)	LENGTH: TYPE: STRANDE			10 amino acid	

	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 26:
Thr	Thr Glu Met Ala Ser Glu Gln G	ly Ala
1	5	10
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 27:
	(i) SEQUENCE CHARACTERISTICS:	/
	<pre>(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:</pre>	9 amino acid linear
	(xi) SEQUENCE DESCRIPTION: SE	
7.7.	Lys Glu Ala Leu Ala Ala Leu L	
1	bys Giu Aia neu Aia Aia neu n 5	ys /
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 28:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	7 amino acid linear
	(xi) SEQUENCE DESCRIPTION: SE	Q ID/NO: 28:
Phe 1	Val Leu Gln Ala Lys Lys 5	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 29:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: (B) TYPE:	21 amino acid
	(C) STRANDEDNESS: (D) TOPOLOGY:	linear
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 29:
Glu 1	Thr Gln Pro Asp Pro Gly Gln I	le Leu Lys Lys Val Pro Met Val 10 15
Ile	Gly Ala Tyr Thr	
(2)	INFORMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 30:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	21 amino acid linear

	(ix) FEATURE:
unkr	(D) OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is nown.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
Xaa 1	Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Glu 5 10 15
Xaa	Gly Xaa Gly Lys
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
77-	Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Glu
1	5 10
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 8 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
	(ix) FEATURE:
	(D) OTHER INFORMATION: Xaa in position 6 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
Lys 1	Leu Glu Phe Leu Xaa Ala Lys
(2)	information por sequence identification number: 33:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 9 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
	(ix) FEATURE:
Bane :	(D) OTHER INFORMATION: Xaa in position 1 is Lysine or

	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 33:
Xaa 1	Val His Gln Val Trp Ala Ala Ly 5	s
(2)	INFORMATION FOR SEQUENCE IDENT	IFICATION NUMBER: 34:
	(i) SEQUENCE CHARACTERISTICS:	
	(B) TYPE: (C) STRANDEDNESS:	14 amino acid
	(ix) FEATURE:	
Arg:	(D) OTHER INFORMATION: X gininel; Xaa in position 11 is u	aa in position 1 is Lysine or nknown.
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 34:
Xaa	a Tyr Ile Phe Phe Met Glu Pro Gl	u Ala Xaa Ser Ser Gly
1	. 5	10/
(2)	INFORMATION FOR SEQUENCE IDENT	IFACATION NUMBER: 35:
,	(i) SEQUENCE CHARACTERISTICS:	
	/	,
	(C) STRANDEDNESS:	14 amino acid linear
	(ix) FEATURE:	
Arg:	(D) OTHER INFORMATION: X sinine; Xaa in position 13 is un	aa in position 1 is Lysine or known.
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO: 35:
Xaa	a Leu Gly Ala Trp Gly Pro Pro Al	a Phe Pro Val Xaa Tyr
1	5	10
(2)	INFORMATION FOR SEQUENCE IDENT	rification number: 36:
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS:	9 amino acid
	(D) TOPOLOGY:	linear
	(1x) FEATURE:	
Arg	(D) OTHER INFORMATION: X ginine.	aa in position 1 is Lysine or
	(xi) SEQUENCE DESCRIPTION: SEC	TD NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37: Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Gly Leu Val Gln Arg (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: ∕amino acid (C) STRANDEDNESS:
(D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38: Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine; Xaa in position 6 is unknown. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39: Xaa Asp Leu Leu Leu Xaa Val

(2)	INFORMAT	ION FOR	SEQUENCE	IDENT	IFICAT	ON NUM	BER:	40:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:						
		LENGTH:	:		39 amino a	aid				
	(C)	STRANDE				icia				
	(D)	TOPOLOG	3Y:		linear					
	(1) ===				·					
			ESCRIPTIO							
Cys 1	Thr Cys	Gly Cys 5	Cys Lys	Cys Cy	s Arg 1	Thr Thr	Cys	Ala Cys 15	Arg	
Cys	Ala Gly	Ala Ala 20	Gly Gly	Thr Cy 2		Thr Cys	Thæ	Cys Cys 30	Thr	
Thr	Cys Thr 35	Cys Ala	Gly Cys							
(2)	INFORMAT	ION FOR	SEQUENCE	IDENT	IFICAT	MUM NO	BER:	41:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:						
	(B)	LENGTH: TYPE: STRANDE TOPOLOG	EDNESS:		24 emino a linear	ncid				
	(xi) SEQ	UENCE DE	SCRIPTIO	n:/seq	ID NO:	41:				
Cys 1	Cys Thr	Cys Gly 5	Cys Thr	Cys Cy	s Thr 1	Thr Cys	Thr	Thr Cys	Thr	
Thr	Gly Cys	Cys Cys 20	Thr Thr	Cys						
(2)	INFORMAT	ION FOR	SEQUENCE	IDENT	IFICATI	ON NUM	BER:	42:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:						
	(B)	LENGTH: TYPE: STRANDE TOPOLOG	EDNESS:	:	60 nucleic single linear	acid				
	(xi) SEQ	UENCE DE	ESCRIPTIO	N: SEQ	ID NO	42:				
AAGT	rgcccaa a	TGAGTTTA	AC TGGTGA	TCGC T	GCCAAA	ACT ACG	TAATO	GC CAGC	TTCTAC	60
(2)/	INFORMAT	ION FOR	SEQUENCE	IDENT	IFICAT]	ON NUM	BER:	43:		
	(i) SEQU	ENCE CHA	ARACTERIS	TICS:						
/	(B) (C)	LENGTH: TYPE: STRANDE	EDNESS:	:	36 nucleio single linear	c acid				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43: 36 AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEOUENCE DESCRIPTION: SEQ ID NO: 44: AAGGCGGAGG AGCTGTACCA GAAGAGAGTG CTGACCATAA CCGGCAT/CTG CATCGCCCTC 60 CTTGTGGTCG GCATCATGTG TGTGGTGGCC TACTGCAAAA CCAAGAAACA GCGGAAAAAG 120 CTGCATGACC GTCTTCGGCA GAGCCTTCGG TCTGAACGAA AGAATATGAT GAACATTGCC 180 AATGGGCCTC ACCATCCTAA CCCACCCCC GAGAATGTCC/AGCTGGTGAA TCAATACGTA 240 TCTAAAAACG TCATCTCCAG TGAGCATATT GTTGAGAGÁG AAGCAGAGAC ATCCTTTTCC 300 ACCAGTCACT ATACTTCCAC AGCCCATCAC TCCACTACTG TCACCCAGAC TCCTAGCCAC 360 AGCTGGAGCA ACGGACACAC TGAAAGCATC CTTTCCGAAA GCCACTCTGT AATCGTGATG 420 TCATCCGTAG AAAACAGTAG GCACAGCAGC ÇCAACTGGGG GCCCAAGAGG ACGTCTTAAT 480 GGCACAGGAG GCCCTCGTGA ATGTAACAGO TTCCTCAGGC ATGCCAGAGA AACCCCTGAT 540 TCCTACCGAG ACTCTCCTCA TAGTGAAAG 569 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDÉDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45: Val His Gln Xal Trp Ala Ala Lys 1 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46: SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear · (ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 10 is unknown.

	(xi) SEQU	JENCE DESCRIPTION: SEG	Q ID NO: 46:
Tyr 1	Ile Phe I	Phe Met Glu Pro Glu Ai 5	la Xaa Ser Ser Gly 10
(2)	INFORMAT	ION FOR SEQUENCE IDEN	rification Number: 47:
	(i) SEQUE	ENCE CHARACTERISTICS:	
	(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	13 amino acid linear
	(ix) FEAT	TURE:	
	(D)	OTHER INFORMATION:	Xaa in position 12 is unknown.
	(xi) SEQ	UENCE DESCRIPTION: SE	Q ID NO: 47:
Leu 1	Gly Ala '	Trp Gly Pro Pro Ala P 5	he Pro Val Xaa Tyr 10
(2)	INFORMAT	ION FOR SEQUENCE IDEN	rrication number: 48:
	(i) SEQUI	ENCE CHARACTERISTICS	/
	(B) (C)	LENGTH: TYPE: STRANDEDNESS:	8 amino acid
	, ,	TOPOLOGY:	linear
		UENCE DESCRIPTION: SE	Q ID NO: 48:
Trp 1	Phe Val	Val Ile Gly Gly Lys 5	
(2)	INFORMAT	ION FOR SEQUENCE IDEN	TIFICATION NUMBER: 49:
	(i) SEQUI	ENCE CHARACTERISTICS:	
	(A) (B) (C)	LENGTH: TYPE: STRANDEDNESS:	15 amino acid
	(D)	TOPOLOGY:	linear
	(xi) SEQ	UENCE DESCRIPTION: SE	Q ID NO: 49:
Ala 1	Ser Pro	Val Ser Val Gly Ser V 5	al Gln Glu Leu Val Gln Arg 10 15
(2)	INFORMAT	ION FOR SEQUENCE IDEN	TIFICATION NUMBER: 50:
	(i) SEQU	ENCE CHARACTERISTICS:	
/	(B)	LENGTH: TYPE:	12 amino acid
		STRANDEDNESS: TOPOLOGY:	linear

	(xi)	SEQ	UENCI	E DE	SCRI	PTION	: SEÇ) ID NO: 5	0:			
Val 1	Cys	Leu :	Leu :	Thr 5	Val 2	Ala A	la Le	eŭ Pro Pro 10	Thr			-/
(2)	INFO	RMAT	ION I	FOR	SEQU	ENCE	IDENT	rification	NUMBER:	5	51: /	,
	(i)	SEQU	ENCE	СНА	RACT	ERIST	CICS:					
		(B) (C)	LENG TYPI STRA TOPG	E :		S:		9 amino aci linear	đ			
	(xi)	SEQ	UENCI	E DE	SCRI	PTION	I: SEÇ	O ID NO: 5	1:			
Lys 1	Val	His	Gln '	Val 5	Trp .	Ala A	la Ly	rs				
(2)	INFO	RMAT	ION I	FOR	SEQU	ENCE	IDENT	rification	NUMBER:	ĩ	52:	
	(i)	SEQU	ENCE	СНА	RACT	ERIST	CICS:					
		(B) (C)	LENG TYPI STRA TOPO	E: ANDE		S:		13 amino aci linear	d			
	(ix)	FEA	TURE	:								
		(D)	OTI	HER	INFO	RMATI	OXI:	Xaa in po	sition 12	2 is	unknow	ı.
	(xi)	SEQ	UENC	E DE	SCRI	PTION	: SEC	Q ID NO: 5	2:			
Lys 1	Ala	Ser	Leu i	Ala 5	Asp	Sex G	ly G	lu Tyr Met 10	Xaa Lys			
(2)	INFO	RMAT	ION I	FOR	SEØU	ENCE	IDENT	rification	NUMBER:		53:	
	(i)	SEQU	ENCE	CHA	RACT	ERIST	CICS:					
		(A) (B) (C) (D)		E;/	DNES	S:		6 amino aci	d			
	(ix)	, ,	TURE		••			11.1041				
	,,	(D),			INFO	RMATI	ON:	Xaa in po	sition 5	is u	unknown	
	(xi)	ŞÆQ	UENC	E DE	SCRI	PTION	I: SE(Q ID NO: 5	3:			
Asp 1	Leu	Leu	Leu :	Xaa 5	Val							
(2)/	INFO	RMAT	'ION I	FOR	SEQU	ENCE	IDENT	rification	NUMBER:	!	54:	
	(i)	SEQU	ENCE	СНА	RACT	ERIST	CICS:					
/												

		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic ac single linear	cid		,
	(ix)	FE	ATURE:				
or T G or		(D) at po	OTHER INFORMATIO	N: N at positi G; N at positi	ions 3, 12 a ions 9 and 1	nd 18 is C 5 is A, T,	!
	(xi)	SEQ	UENCE DESCRIPTION:	SEQ ID NO: 54	4 :		
TTNA	ANGG	NG AI	NGCNCANAC			20)
(2)	INFO	RMAT:	ION FOR SEQUENCE I	DENTIFICATION	NUMBER:	55:	
	(i)	SEQUI	ENCE CHARACTERISTI	CS:			
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	21 nucleic ac single linear	cid		
	(ix)	FE	ATURE:				
N at	-	(D) itio	OTHER INFORMATIOns 4, 10, and 16 i	N: N at posits A or G; N at	tions 7 and position 1	13 is C or 9 is A, T,	T,
	(xi)	SEQ	JENCE DESCRIPTION;	SEQ ID NO: 55	5:		
CATN	TANT	CN T	ANTCNTCNG C			21	
(2)	INFO	RMAT:	ION FOR SEQUENCE I	DENTIFICATION	NUMBER:	56:	
	(i)	SEQUI	ENCE CHARACTERISTI	CS:			
		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic ac single linear	cid		
	(ix)	FE	ATURE:				
N at	pos	(D) itio	OTHER INFORMATIONS 6, 9, and 18 is	N: N at posit A, T, G or C.	cions 3 and	15 is C or	Т,
	(xi)	SEQ	UENCE DESCRIPTION:	SEQ ID NO: 56	5:		
TGNT	'CNGA	NG CO	CATNTCNGT			20)
(2)	INFO	RMAT:	ION FOR SEQUENCE I	DENTIFICATION	NUMBER:	57:	
,	(i)	SEQUI	ENCE CHARACTERISTI	CS:			
		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic ac single linear	cid		

(ix) FEATURE: (D) OTHER INFORMATION: N at positions 3 and 14 is C or T; N at position 6 is A or G; N at positions 9 and 17 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57: 20 TGNTCNCTNG CCATNTCNGT (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: nucleic acid (B) TYPE: single (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at position 3 is A, G or T; N at position 18 is C or T; N at positions 6, 12, and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: \$8: CCNATNACCA TNGGNACNTT 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at position 12 is C or T; N at position 15 is A or G; X at positions 3, 9 and 18 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59: GCNGCCCANA CYTGRTGNAC 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 60: (i) SEQUENCE CHARACTERISTICS: (A) /LENGTH: 20 (B) TYPE: nucleic acid (Ø) STRANDEDNESS: single (D) TOPOLOGY: linear FEATURE: (ix) (D) OTHER INFORMATION: N at positions 3 and 9 is C or T; N at positions 5 and 8 is A or G; N at position 6 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

20 GCNTCNGGNT CCATNAANAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid single (C) STRANDEDNESS: linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at position 6 is A/G or T; N at position 3 is C or T; N at position 15 is A or G; N at positions 9 and 11 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61: 20 CCNTCNATNA CNACNAACCA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 (B) TYPE: nuclei¢ acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 6 and 9 is A or G; N at positions 3, 11 and 14 is A/T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62: 17 TCNGCNAANT ANCCNGC (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63: (i) SEQUENCE CHARACTÉRISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEONESS: single (D) TOPOLOGY: linear (ix) FEATURE/ OTHER INFORMATION: N at positions 12 and 15 is C or T; N at positions/3, 6, 9 and 17 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63: GCNGCNAGNG/CNTCNTTNGC 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64: SEQUENCE CHARACTERISTICS:

(A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at positions 6, 12 and 15 is of or T; N at positions 3, 9, and 18 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64: 20 GCNGCNAANG CNTCNTTNGC (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: 20 (A) LENGTH: nucleic acid (B) TYPE: (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 3 and 9 is C or T; N at position 18 is A or G; N at positions 6, 12 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65: 20 TTNTTNGCNT GNAGNACNAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 nucleic acid (B) TYPE: (C) STRANDEDNESS single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 3, 9 and 12 is C or T; N at position 18 is A or G; N at positions 6 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66: TTNTTNGCNT GNAANACNAA 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear FEATURE: (ix/)

(D) OTHER INFORMATION: N at positions 9 and 12 is C or T; N at positions 3, 6 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67: 17 TGNACNAGNT CNTGNAC (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68: (i) SEQUENCE CHARACTERISTICS: 17 . (A) LENGTH: (B) TYPE:(C) STRANDEDNESS: nucleic acid single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at positions 6, 9, and 12 is C or T; N at positions 3 and 15 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: \$8: TGNACNAANT CNTGNAC 17 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69: (i) SEQUENCE CHARACTERISTICS: 21 (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N at position 7 is C or T; N at positions 4 and 16 is A or G; N at positions 10, 13 and 19 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69: CATNTANTON CONGANTONG C 21 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70: (i) SEQUENCE CHARACTERISTICS: LENGTH: 21 (B') TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear FEATURE: (D) OTHER INFORMATION: N at position 7 is C or T; N at positions 4, 13 and 16 is A or G; N at positions 10 and 19 is A, T, & or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

(2)	INFOR	MATI	ON F	OR SE	QUENCE	E IDEN'	rificati	ON NUM	BER:	71:		
	(i) S	EQUE	ENCE	CHARA	CTERIS	STICS:						/
		(B) (C)		:	ESS:		21 nucleic single linear	acid				
	(ix)	FEA	ATURE	:					/	/		
N at G or	posi C.	(D) tion	OTH n 4 i	ER IN	FORMAT	TION: I	N at pos ositions	itions 1, 7,	10 and 13 and	19 16	is C is A	or T;
	(xi)	SEQU	JENCE	DESC	RIPTIO	ON: SE	Q ID NO:	71:/	,			
NGAN	TCNGC	'N AA	ANGAN	GCNT	т							21
(2)	INFOR	MATI	ON F	OR SE	QUENCI	E IDEN	TIFICATI	ON NUM	BER:	72:		
	(i) S	EQUE	ENCE	CHARA	CTERIS	STICS:						
		(B) (C)			ESS:	/	21 nucleic single linear	acid				
	(ix)	FEA	ATURE	:								
posi G or	tion C.	(D) 4 is	OTH A o	ER IN	FORMAT N at 1	ZION: 1	N at pos ons 1, 7	ition , 10,	19 is C 13 and	or 16 i	T; N s A,	at T,
	(xi)	SEQU	JENCE	DESC	RIPTIO	ON: SE	Q ID NO:	72:				
NGAN	TCNGC	'N AC	engan	GCNT	Т							21
(2)	INFOR	(TAM	ON F	OR SE	QUENCI	E IDEN	TIFICATI	ON NUM	BER:	73:		
	(i) S	EQUE	encæ	CHARA	CTERIS	STICS:						
		(A) (B)/ (C) (D)			ESS:		21 nucleic single linear	acid				
	(ix)/	FE#	ATURE	::								
	posi or C						N at pos N at po					
	(xi)	SEQU	JENCE	DESC	RIPTIO	ON: SE	Q ID NO:	73:				
NCTN	TCNGC	N A	ANGAN	GCNT	т							21
(2)	INFOR	(TAM	ION F	OR SE	QUENCI	E IDEN	TIFICATI	ON NUM	BER:	74:		

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	21 nucleic acid single linear
(ix) FEATURE:	. /
(D) OTHER INFORMATION: No positions 1 and 14 is A or G ; N at A, T, G or C .	at position 19 is C or T; N at positions 7, 10, 13 and 16 is
(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 74:
NCTNTCNGCN AGNGANGCNT T	21
(2) INFORMATION FOR SEQUENCE IDENT	rification number: 75:
(i) SEQUENCE CHARACTERISTICS:	
	21 nucleid acid single linear
(ix) FEATURE:	
(D) OTHER INFORMATION: No at positions 4 and 13 is A or G, A, T, G or C.	at positions 10 and 19 is C or T; N at positions 1, 7 and 16 is
(xi) SEQUENCE DESCRIPTION; SEQ) ID NO: 75:
NGANTCNGCN AANCTNGCNT T	21
(2) INFORMATION FOR SEQUENCE IDENT	CIFICATION NUMBER: 76:
(i) SEQUENCE CHARACTERISTICS:	,
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	21 nucleic acid single linear
(ix) FEATURE:	
(D) OTHER INFORMATION: positions 4 and 13 is A or G; N at A, T, G or 9.	N at position 19 is C or T; N at positions 1, 7, 10 and 16 is
(xi) SEQUENCE DESCRIPTION: SEC) ID NO: 76:
NGANTCNOCN AGNCTNGCNT T	21
(2) INFORMATION FOR SEQUENCE IDEN:	rification number: 77:
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS:	730 nucleic acid

(D) TOPOLOGY:

linear

- (ix) FEATURE:
 - (D) OTHER INFORMATION:
- GTATGTGTCA GCCATGACCA CCCCGGCTCG TATGTCACCT GTAGATTTCC ACACGCCAAG 60
 CTCCCCCAAA TCGCCCCCTT CGGAAATGTC TCCACCCGTG TCCAGCATGA CGGTGTCCAT 120
 GCCTTCCATG GCGGTCAGCC CCTTCATGGA AGAAGAGAGA CCTCTACTTC TCGTGACACC 180
 ACCAAGGCTG CGGGAGAAGA AGTTTGACCA TCACCCCTCAG CAGTTCAGCT CCTTCCACCA 240
 CAACCCCGCG CATGACAGTA ACAGCCTCCC TGCTAGCCCC TTGAGGATAG TGGAGGATGA 300
 GGAGTATGAA ACGACCCAAG AGTACGAGCC AGCCCAAGAG CCTGTTAAGA AACTCGCCAA 360
 TAGCCGGCGG GCCAAAAGAA CCAAGCCCAA TGGCCACATT GCTAACAGAT TGGAAGTGGA 420
 CAGCAACACA AGCTCCCAGA GCAGTAACTC AGAGAGTGAA ACACAAGAT TGGAAGTAGG 480
 TGAAGATACG CCTTTCCTGG GCATACAGAA CCCCCTGGCA GCCAGTCTTG AGGCAACACC 540
 TGCCTTCCGC CTGGCTGACA GCAGGACTAA CCCCAGCAGG CGCTTCTCGA CACAGGAAGA 600
 AAATCAAGCC AGGCTGTCTA GTGTAATTGC TAACCAAACAC CCTATTGCTG TATAAAACCT 660
 AAATAAACAA TTAATAAACAA 730
- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

21

(B) TYPE:

nucleic acid

(C) STRANDEDNESS,

single

(D) TOPOLOGY:

linear

- (ix) FEATURE:
- (D) OTHER INFORMATION: N at positions 10 and 19 is C or T; N at positions 1, 4 and 13 is A or G; N at positions 7 and 16 is A, T, G or C.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

NCTNTCNGCN AAMCTNGCNT T

21

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

21

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:
(D) TOPOLOGY:

single linear

(ix) FEATURE:

LAL, I DITTORD.

(D) OTHER INFORMATION: N at position 19 is C or T; N at positions 1, 4 and 13 is A or G; N at positions 7, 10 and 16 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79: 21 NCTNCTNGCN AGNCTNGCNT T (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 nucleic acid (B) TYPE: single (C) STRANDEDNESS: linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at position 9 is A or G; N at positions 3, 6, 17 and 18 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO; 80: 20 ACNACNGANA TGGCTCNNGA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 nucleic acid (B) TYPE: (C) STRANDEDNESS: single linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at position 16 is C or T; N at position 9 is A or G/, N at positions 3, 6 and 17 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81: 20 ACNACNGANA TGGCAGNNGA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (½x) FEATURE: (D) OTHER INFORMATION: N at position 3 is C or T; N at position 6 is A or G; N at positions 9, 15 and 18 is A, T, G or C. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

20 CANCANGTNT GGGCNGCNAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEDNESS: single linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N at position 3 is Cor T; N at position 15 is A or G; N at positions 9, 15 and 18 is/A, T, G or C; N at position 12 is A, C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83: 20 TTNGTNGTNA TNGANGGNAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucletic acid sing/le (C) STRANDEDNESS: (D) TOPOLOGY: limear (ix) FEATURE: (D) OTHER INFORMATION: /N at positions 9 and 15 is C or T; N at position 3 is A or G; N at positions 6, 12 and 18 is A, T, G or C. (xi) SEQUENCE DESCRIPTION / SEQ ID NO: 84: AANGGNGANG CNCANACNGA 20 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURÉ: (D) ϕ THER INFORMATION: N at positions 7 and 15 is C or T; N at position/3 is A or G; N at positions 6, 9, 11, 14 and 17 is A, T, G or C/ (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GANGCNNTNG CNGCNNTNAA

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

129

20

	(1)	EQUI	ENCE CHARACTERISTICS:		
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear	/
	(ix)	FE	ATURE:		
posi A, T		s 15	OTHER INFORMATION: and 18 is A or G; N	N at position 19 is at positions 3, 6, 9	C Or T; N at and 12 is
	(xi)	SEQ	JENCE DESCRIPTION: SE	Q ID NO: 86:	
GTNG	GNTCI	NG TI	NCANGANNT		20
(2)	INFO	RMAT:	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	87:
	(i) s	SEQUI	ENCE CHARACTERISTICS:		
		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	20 nucleic acid single linear	
	(ix)	FE	ATURE:		
N at A, T			OTHER INFORMATION: ns 15 and 18 is A or	N at positions 9 ar G N at positions 3,	nd 19 is C or T 6 and 12 is
	(xi)	SEQ	JENCE DESCRIPTION: SE	Q ID NO: 87:	
GTNG	GNAGI	NG TI	NCANGANNT		20
(2)	TNFOI	ЗМДТ.	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	88:
(-,			ENCE CHARACTERISTICS:		
		(B)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	21 nucleic acid single linear	
	(ix)	FE	ATURE		
or T A, T	; N a	(D) at po or C	OTHER INFORMATION: osition 12 is A or G; N at position 13 is	N at positions 4, 7 N at positions 1, 1 A, G or T.	and 16 is C 0 and 19 is
	(xi)	SEØ	/ UENCE DESCRIPTION: SE	Q ID NO: 88:	
NACN	TTNT	IN AI	NNATNTGNC C		21
(2)	INFO	, RMAT:	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	89:
	(j) :	SEQU	ENCE CHARACTERISTICS:		
/	/	(B)	LENGTH: TYPE: STRANDEDNESS:	417 nucleic acid single	

	(ix)		TOI ATURI		GY:			1:	inea	r							/
and	135	(D) is u) Oʻ unkno		INF	ORMA'	rion	: X	aa i	n pos	sitio	ons :	14,	23, 9	90, 1	00, :	12/6,
	(xi)	SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID N): 8	9:						•
TCTA										le I					GA AX aa Asi 1	n Ile	
														cge Arg			101
														GTG Val			149
														GTG Val			197
TCA Ser 65	AAC Asn	GGT Gly	AAG Lys	AGA Arg	TGC Cys 70	CTA Leu	CTG Leu	CGT Arg	GCT Ala	ATT Ile	TCT Ser	CAG Gln	TCT Ser	CTA Leu	AGA Arg 80		245
														TCT Ser 95			293
														TGT Cys			341
														GGT Gly			389
						TAG/ Xa/a 1/35		ATT Ile	Т								417
(2)	INFO	ORMAT	пои	FOR	SEQ	, JENCI	E IDI	ENTI	FICA	rion	NUME	BER:	9	90:			
	(i)	SEQU	JENCI	сн,	RACT	reris	STICS	3:									
		(B) (C)	LEN TYI STI	PÉ: RANDI	EDNES	SS:		s	-		cid						
	(ix)	FE	YURI	፭:													
in p	osit	(I) igh	22 d	THER can b	INFO	ORMA Or (CION 3; N	: N in p	in posit	posit	cion 28 d	16 can l	can l oe C	oe A or T	or G	; N	
	(xi)	/						SEQ :		0: 90):						
CCGA	ATTO	CTG (CAGG	NACU	JC AI	1CCU	BANC	C UGO	3						33	3	
(2)	VNEC	יעשמי	וו ווי	FOD	SEO1	TENICI	וחד ק	י דידואיב	דריאי	rton	MITME	DED.		01.			

	(i) S	EQUENCE CHARAC	TERISTICS:			
		(A) LENGTH: (B) TYPE: (C) STRANDEDNE (D) TOPOLOGY:		37 nucleic acid single linear		
	(ix)	FEATURE:				
posi	tion.	(D) OTHER INF 26 can be A, G		N in position	17 can be A or	Ø; N in
	(xi)	SEQUENCE DESCR	RIPTION: SE	Q ID NO: 91:		
AAGG	ATCCI	'G CAGUGTNTAU 6	GCUCCNATUA	CCATUGG		37
(2)	INFOR	MATION FOR SEC	QUENCE IDEN	TIFICATION NUMB	SER 2 92:	
	(i) S	EQUENCE CHARAC	CTERISTICS:	/		
		(A) LENGTH: (B) TYPE: (C) STRANDEDNE (D) TOPOLOGY:	ESS:	34 nucleic acid single linear		
	(ix)	FEATURE:				
posi	tion	(D) OTHER INF 28 can be A or	FORMATION: GG; N in p	N in position osition 31 can	19 can be C or be C or T.	T; N in
	(xi)	SEQUENCE DESCR	RIPTION: SE	Ø ID NO: 92:	•	
CCGA	ATTCI	G CAGGCUGANT (CUGGUGANTA	NATG		34
(2)	INFO	MATION FOR SEC	QUENCE IDEN	TIFICATION NUMB	BER: 93:	
	(i) S	EQUENCE CHARAC	CTER/ISTICS:			
		(A) LENGTH: (B) TYPE: (C) STRANDEDYE (D) TOPOLOGY:	ESS:	33 nucleic acid single linear		
	(ix)	FEATURE:				
		(D) OTHER INE 22 can be C or C or T.	FORMATION: c T; N in p	N in position osition 28 can	19 can be C or be A or G; N i	T; N in n position
	(xi)	SEQUENCE DESCR	RIPTION: SE	Q ID NO: 93:		
CCGF	ATTC	rg Caggcugana (ENGGUGANTA	NAT		33
(2)	INFO	/ MATION FOR SEQ	QUENCE IDEN	TIFICATION NUME	BER: 94:	
	(i) s	EQUENCE CHARAC	CTERISTICS:			
,		(A) LENGTH: (B) TYPE: (C) STRANDEDNE	ESS:	34 nucleic acid single		

		(D) TOPOLOGY:	linear	
	(ix)	FEATURE:		
posi	tion	(D) OTHER INFORMATION: 22 can be C or T; N in p	N in position 19 can be A or osition 32 can be A or G.	G; N in
	(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO: 94:	
AAGG	SATCCI	TG CAGUUUCATN TANTCUCCUG	ANTC	34
(2)	INFOR	RMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 95:	
	(i) S	SEQUENCE CHARACTERISTICS:		
		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	34 nucleic acid single linear	
	(ix)	FEATURE:		
			N in position 20 can be A or osition 29 can be A or G; N in	
	(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO. 95:	
AAGG	ATCCI	TG CAGUUUCATN TANTCUCCNC	TNTC	34
(2)	INFOR	RMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 96:	
	(i) S	SEQUENCE CHARACTERISTICS!	,	
		(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	33 nucleic acid single linear	
	(ix)	FEATURE:		
posi	tion	(D) OTHER INFORMATION: 19 can be A or G.	N in position 16 can be C or	T; N in
	(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO: 96:	
CCGI	AATTCI	rg cagcarcang tutgggcugc	TAA	33
(2)	INFO	RMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 97:	
	(i) }	SEQUENCE CHARACTERISTICS:		
		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	35 nucleic acid single linear	
	/(ix)	FEATURE:		
/				

				1
N in posi	pos: tion	(D) OTHER INFORMATION: ition 19 can be C or T; N 28 can be A or G; N in p	N in position 16 can be A or in position 22 can be C or T osition 34 can be A or G.	C or T;
	(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO: 97:	
CCGA	ATTC'	TG CAGATNTTNT TNATGGANCC	UGANG	35
(2)	INFO	RMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 98:	
	(i) :	SEQUENCE CHARACTERISTICS:		
		(A) LENGTH:(B) TYPE:(C) STRANDEDNESS:(D) TOPOLOGY:	nucleic acid single linear	
	(ix)	FEATURE:		
		(D) OTHER INFORMATION:	N in position 30 can be C or	т.
	(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO: 98/:	
CCGA	ATTC'	TG CAGGGGGUCC UCCUGCUTTN	CCUGT	35
(2)	INFO	RMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 99:	
	(i)	SEQUENCE CHARACTERISTICS:		
		(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	33/ nucleic acid single linear	÷
	(ix)	FEATURE:		
posi	tion.	(D) OTHER INFORMATION: 28 can be A or C or T; N	N in position 19 can be C or in position 31 can be A or G	T; N in
	(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO: 99:	
CCGA	ATTC'	TG CAGTGGTTNG TUCTUATNGA	NGG	33
(2)	INFO	RMATION FOR SEQUENCE IDEN	TIFICATION NUMBER: 100:	
	(i)	SEQUENCE CHARACTERISTICS:		
		(A) LENGTH: (B) TYPE: (C) STEANDEDNESS: (D) TOPOLOGY:	34 nucleic acid single linear	
	(ix)	FEATURE:		
Inos	sinc.	(D) OTHER INFORMATION: Y can be cytidine or thy	N at position 17, 20, and 26 midine.	5 is
	(xi)/	SEQUENCE DESCRIPTION: SE	Q ID NO: 100:	
AAGG	/	TG CAGYTTNGC NGCCCANACY T		34

(2)	TNFO	MAT.	ION FOR SEQUENCE IDEN	rificatio	ON NUMBER:	101:	
(2)			ENCE CHARACTERISTICS:			/	
	(1)	(A) (B) (C)	LENGTH: TYPE: STRANDEDNESS:	33 nucleic single linear	acid		
	(ix)	FEA!	rure:				
	tion can be	22 (OTHER INFORMATION: can be C or T; N in poor G.	N in pos osition 2	sition 16 can 28 can be A c	be C or or G; N in	T; N in n position
	(xi)	SEQ	JENCE DESCRIPTION: SEC	Q ID NO:	101:		
AAGG	SATCC	rg cz	AGGCNTCUG GNTCCATNAA 1	NAA			33
(2)	INFO	RMAT:	ION FOR SEQUENCE IDEN'	rificatio	N NUMBER:	102:	
	(i) SEQUENCE CHARACTERISTICS:						
		(B) (C)		33 nucleic single linear	acid		
	(ix)	FEA:	TURE:				
		(D)	OTHER INFORMATION:	N in posi	ition 19 can	be A or (3.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:						
AAGG	BATCC	rg cz	AGACUGGNA AUGCUGGUGG	UCC			33
(2)	TNEO	ייי איי	ION FOR SEQUENCE IDEN	PT PT ("A TT (M MIMPED.	102.	
(2)	2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103: (i) SEQUENCE CHARACTERISTICS:						
	(1)	(A) (B) (C)	LENGTH: TYPE: STRANDEPNESS: TOPOLOGY:	35 nucleic single linear	acid		
	(ix)	FEA:	rure: /				
posi posi	ition ition	(D) 20 (32 (OTHER INFORMATION: I can be C or T; N in pocan be A or G.	N in posi osition 2	ition 14 can 23 can be A c	be C or T	Γ; N in ; N in
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO:	103:		
AAGO	BATCC'	rg o	AGNTTUCCN TCNATUACUA	CNAAC			35
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:						
	(i) SEQUENCE CHARACTERISTICS:						
		(B)	LENGTH: TYPE: STRANDEDNESS:	33 nucleic single	acid		

linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: N in position 4 can be A or G; N in position 7 cna be C or T; N in position 10 can be A or G; N in position 13 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104: CATNTANTCN TANTCTCUGC AAGGATCCTG CAG 33 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic ac/d (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N in position 16 can be A or G; N in position 22 can be C or T; N in position 28 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ 1/D NO: 105: CCGAATTCTG CAGAANGGUG ANGCUCANAC UGA 33 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106: (i) SEQUENCE CHARACTERISTACS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER LANFORMATION: N in position 6 can be C or T; N in position 12 can be C or T; N in position 15 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106: GCUGCNAAUG CNTCN/TUGC AAGGATCCTG CAG 33 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 √B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: N in position 12 can be C or T; N in position 15 can be C or T. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ix) FEATURE:
(D) OTHER INFORMATION: N in position 6 can be A or G; N in position 9 can be A or G.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:
TCUGCNAANT AUCCUGCAAG GATCCTGCAG 30
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 38 nucleic acid single linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:
CATCGATCTG CAGGCTGATT CTGGAGAATA TATGTGCA 38
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:
AAGGATOCTG CAGCCACATC TCGAGTCGAC ATCGATT 37
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATC	GACA 3'	7/
(2) INFORMATION FOR SEQUENCE IDENTIFE	ICATION NUMBER: 112:	
(i) SEQUENCE CHARACTERISTICS:		
(C) STRANDEDNESS: sir	cleic acid	
(xi) SEQUENCE DESCRIPTION: SEQ II	D NO: 112:	
CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTC	GCAC 3	7
(2) INFORMATION FOR SEQUENCE IDENTIF	ICATION NUMBER: 113:	
(i) SEQUENCE CHARACTERISTICS:		
(C) STRANDEDNESS: sin	cleic acid ngle near	
(xi) SEQUENCE DESCRIPTION: SEQ II	D NO: 113:	
AAGGATCCTG CAGTATATTC TCCAGAATCA GCCA	AGTG 3	7
(2) INFORMATION FOR SEQUENCE IDENTIFE	ICATION NUMBER: 114:	
(i) SEQUENCE CHARACTERISTICS:		
(C) STRANDEDNESS: sin	cleic acid ngle near	
(xi) SEQUENCE DESCRIPTION: SEQ II	D NO: 114:	
AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA	A 3	4
(2) INFORMATION FOR SEQUENCE IDENTIF	ICATION NUMBER: 115:	
(i) SEQUENCE CHARACTERISTICS:		
(C) STRANDEDNESS: sin	cleic acid ngle near	
(xi) SEQUENCE DESCRIPTION: SEQ II	D NO: 115:	
CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAG	GC 3	5
(2) INFORMATION FOR SEQUENCE IDENTIF	ICATION NUMBER: 116:	
(i) SEQUENCE CHARACTERISTICS:	•	

		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	33 nucleic acid single linear		.*
	(xi)	SEQU	JENCE DESCRIPTION: SEG	Q ID NO: 116:		
CATC	CCGGG	BA TO	GAAGAGTCA GGAGTCTGTG (gCA /	/	33
(2)	INFOR	TAMS	ION FOR SEQUENCE IDENT	rification number:	117:	
	(i) S	EQUI	ENCE CHARACTERISTICS:			
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	nucleic acid single linear		
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NØ: 117:		
ATAC	CCGGC	GC TO	GCAGACAAT GAGATTTCAC	ACACCTGCG		39
(2)	INFOR	RMAT	ION FOR SEQUENCE IDEN	rification number:	118:	
	(i) S	EQUI	ENCE CHARACTERISTICS:	•		
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	36 nucleic acid single linear		
	(xi)	SEQ	UENCE DESCRIPTION: SEG	Q ID NO: 118:		
AAGG	ATCCT	rg cz	AGTTTGGAA CCTGCCACAG	ACTCCT		36
(2)	INFOR	TAMS	ion for sequence ident	TIFICATION NUMBER:	119:	
	(i) S	SEQUI	ENCE CHARACTERISTICS:			
		(B) (C)	LENGTH: TYPE: STRANDEDNESS: TOPOLOGY:	39 nucleic acid single linear		
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 119:		
ATAC	ccgg	3 с т	GCAGATGAG ATTTCACACA	CCTGCGTGA		39
(2)	INFO	RMAT	ION FOR SEQUENCE IDEN	TIFICATION NUMBER:	120:	
/	/ (i) s	SEQU:	ENCE CHARACTERISTICS:			
			LENGTH:	12		
		(C)	TYPE: STRANDEDNESS: TOPOLOGY:	amino acid linear		
	(xi)	SEQ	UENCE DESCRIPTION: SE	Q ID NO: 120:		

His 1	Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys 5 10
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 16 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:
Gly 1	Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn 5 10 15
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 13 amino acid linear
	(ix) FEATURE:
	(D) OTHER INFORMATION: Xaa in position 12 is unknown.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:
Leu 1	Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr 5 10
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 23 (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:
Leu 1	Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
Cys	Gly Arg Leu Lys Glu Asp 20
(2)/	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:
	(i) SEQUENCE CHARACTERISTICS:
/	(A) LENGTH: 13 (B) TYPE: amino acid (C) STRANDEDNESS:

		(D)	TOP	OLOG	Υ:			linear	c				
	(ix)	FEA	TURE	:									/
		(D)	ro	HER	INFO	RMAT	ON:	Xaa ir	n posi	ltion	10 i	s unkn	own.
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	1: SEÇ	ON DI O	D: 124	l :		/	
Tyr 1	Ile	Phe	Phe	Met 5	Glu	Pro (3lu Al	la Xaa 10	Ser S	er G	ly		
(2)	INFO	RMAT	ON	FOR	SEQU	JENCE	IDENT	rifica:	rion 1	NUMBE!	R : /	125:	
	(i)	SEQU	ENCE	сна	RACT	ERIST	rics:			/			
		(B) (C)	TYE STE	IGTH: PE: RANDE POLOG	DNES	SS:		23 amino linear					
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	1: SEÇ	ON DI Q	D: / 25	5:			
Lys 1	Glu	Asp	Ser	Arg 5	Tyr	Ile 1	Phe Ph	ne Met	Glu I	?ro G	lu Al	a Asn 15	Ser
Ser	Gly	Gly	Pro 20	Gly	Arg	Leu							
(2)	INFO	RMAT	CION	FOR	SEQU	JENCE	IDEN	rifica:	rion i	NUMBE:	R:	126:	
	(i)	SEQU	ENCE	CHA	RACT	ERIS	rics:						
		(B) (C)	TYI STF	IGTH: PE: RANDE POLOG		ss:/		14 amino linear					
	(xi)	SEÇ	UENC	CE DE	SCRI	PTIOI	N: SE(O ID NO	D: 126	5:			
Val 1	Ala	Gly	Ser	Lys 5	Levi	Val 1	Leu Ai	rg Cys 10	Glu 7	fhr S	er Se	r	
(2)	INFO	RMAT	CION	FOR	SEQU	JENCE	IDEN	rifica:	TION 1	NUMBE:	R:	127:	
	(i)	SEQU	JENCE	E/CHA	RACI	ERIS	rics:						
		(A) (B) (C) (D)	TYT STF	/ IGTH: PE: RANDE POLOG	DNES	SS:		16 amino linea:					
	(xi)	SEC	UENC	CE DE	SCRI	PTIO	N: SE	O ID N	O: 12	7:			
Glu 1	Tyr	Lys	Cys	Leu 5	Lys	Phe 1	Lys T	rp Phe 10	Lys 1	Lys A	la Th	r Val 15	Met
(2)	INFO	RMAI	NOI	FOR	SEQU	JENCE	IDEN	rifica'	TION 1	NUMBE	R:	128:	
	(i)	SEQU	JENCI	E CHA	RACI	TERIS'	rics:						

	/
(A) LENGTH: (B) TYPE:	26 amino acid
(C) STRANDEDNESS: (D) TOPOLOGY:	linear
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 128:
Cys Glu Thr Ser Ser Glu Tyr Ser 1 5	Ser Leu Lys Phe Lys 10 15
Asn Gly Ser Glu Leu Ser Arg Lys 20	Asn Lys 25
(2) INFORMATION FOR SEQUENCE ID	ENTIFICATION NUMBER: 129:
(i) SEQUENCE CHARACTERISTIC	s:
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	13 amino acid linear
(ix) FEATURE:	
(D) OTHER INFORMATION	: Xaa in position 12 is unknown.
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 129:
Lys Ala Ser Leu Ala Asp Ser Gly 1 5	Giu Tyr Met Xaa Lys 10
(2) INFORMATION FOR SEQUENCE D	ENTIFICATION NUMBER: 130:
(i) SEQUENCE CHARACTERISTIC	S:
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	23 amino acid linear
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 130:
Glu Leu Arg Ile Ser Lys Ala Ser 1	Leu Ala Asp Ser Gly Glu Tyr Met 10 15
Cys Lys Val Ile Ser Lys Leu 20	
(2) INFORMATION FOR SEQUENCE ID	DENTIFICATION NUMBER: 131:
(i) SEQUENCE CHARACTERISTIC	CS:
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:	12 amino acid linear
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 131:
Ala Ser Leu Ala Asp Glu Tyr Glu 1 5	1 Tyr Met Arg Lys 10

(2)	INFO	ORMAT	rion	FOR	SEQU	JENCE	E IDE	ENTIE	FICAT	CION	NUME	BER:	1	.32:/				
(-/			JENCE															
	, - ,	(A) (B) (C)	LEN TYI	IGTH : PE : RANDE	: EDNES			22 ar	2 mino inear		ì			/				
	, ,,	, ,	TOI			- DM - C	NT (,						
			QUENC									~/			G			
Leu 1	Arg	Ile	Ser	Lys 5	Ala	Ser	Leu	Ala	Asp 10	Ser	GIY /	G/Lu	Tyr	мет 15	Cys			
Lys	Val	Ile	Ser 20	Lys	Leu													
(2)	INF	ORMA!	rion	FOR	SEQU	JENCI	E IDE	ENTI	FICAT	LION	NUMI	BER:	:	133:				
	(i)	SEQ	JENCI	E CHA	ARACT	CERIS	STICS	3:										
		(B)	LEI TYI STI	PE: RANDI	EDNES	SS:		nı s:	14 iclei ingle inean	9	cid					,		
	(xi)) SE(QUENC	CE DI	ESCR	PTIC	ON: S	SEQ/	ID NO): 13	33:							
CCT	GCAG	CAT His 1	CAA Gln	GTG Val	TGG Trp	GCG Ala 5	GCG Ala	AAA Lys	GCC Ala	GGG Gly	GGC Gly 10	TTG Leu	AAG Lys	AAG Lys	GAC Asp	TCG Ser 15	CTG Leu	55
CTC Leu	ACC Thr	GTG Val	CGC Arg 20	CTG Leu	GGC Gly	GCC Ala	TGG Trp	GGC Gly 25	CAC His	CCC Pro	GCC Ala	TTC Phe	CCC Pro 30	TCC Ser	TGC Cys	103		
GGG Gly	CGC Arg	CTC Leu 35	AAG Lys	GAG Glu	GAC Asp	AGC Ser	AGG Arg 40	TAC Tyr	ATC Ile	TTC Phe	TTC Phe	ATG Met 45	GAG Glu	CCC Pro	GAG Glu	151		
GCC Ala	AAC Asn 50	AGC Ser	AGC Ser	GGC Gly	GGG/ Gly	CCC Pro 55	GGC Gly	CGC Arg	CTT Leu	CCG Pro	AGC Ser 60	CTC Leu	CTT Leu	CCC Pro	CCC Pro	199		
	CGA Arg															247		
	CGG Arg															295		
	GTG Val						Val					Thr				343		
	TCC Ser/															391		
	AAG Lys 130															439	•	

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr 155 150 ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn 170 165 ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG/CGT GCT ATT Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leú Arg Ala Ile 190 185 TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT/CAC ACT 625 Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr 200 TGAATCACGC AGGTGTGTGA AATCTCATTG TCAACAAATA AAAATCATGA AAGGAAAAAA 685 AAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC 744 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: 11**9**3 (A) LENGTH: nwcleic acid (B) TYPE: (C) STRANDEDNESS: #ingle (D) TOPOLOGY: /linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134: CCTGCAG CAT CAA GTG TGG GCG GQG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55 His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TGC 103 Leu Thr Val Arg Leu Gly A/a Trp Gly His Pro Ala Phe Pro Ser Cys 25 20 GGG CGC CTC AAG GAG GAC/AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 151 Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu 40 35 GCC AAC AGC AGC GGC GGG CCC GGC CTT CCG AGC CTC CTT CCC CCC 199 Ala Lys Ser Ser Gly/Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247 Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gln Pro Gly Ala Val CAA CGG TGC GOC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 295 Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu 85 TCT GTG GCA/GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343 Ser Val Alá Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu 100 105 TAC TCC ICT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 391 Tyr Ser/Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser 120

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439 Arg Lys Asn Lys Gly Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys 130 135 TCA GGA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 487 Ser Gly Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr 150 ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 535 Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Sér Ala Asn ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT AÇÁ GCT GGG ACA 583 Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr 190 180 185 AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA AÇT TTC TGT GTG AAT 631 Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 200 205 195 GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 679 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr 210 215 220 TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 727 Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn 235 225 GTG CCC ATG AAA GTC CAA ACC CAA GAA/AGT GCC CAA ATG AGT TTA CTG 775 Val Pro Met Lys Val Gln Thr Gln Gly Ser Ala Gln Met Ser Leu Leu 250 GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC 826 Val Ile Ala Ala Lys Thr Thr 260 CCTTTCTGTC TCTGCCTGAA TAGCGQATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC 886 TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT 946 GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT 1006 GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT 1066

ACTGTGATAC GACATGATAC TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA 1126 GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC 1186

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135
 - (i) SEQUENCE CHARACTERISTICS:
 - (A)/LENGTH: 1108 base pairs
 - (B/ TYPE: nucleic acid
 - (¢) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - √ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:

TCTAGAG

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 8...778
- (D) OTHER INFORMATION:

1193

(:	xi) S	EQUE	ENCE	DESC	CRIPT	CION:	: SEC	O ID	NO:	135:				/	
CCTGCAG	CAT His 1	CAA Gln	GTG Val	TGG Trp	GCG Ala 5	GCG Ala	AAA Lys	GCC Ala	GGG Gly	GGC Gly 10	TTG Leu	AAG Lys	AAG Lys	GAC Asp	49
TCG CTG Ser Leu 15	CTC Leu	ACC Thr	GTG Val	CGC Arg 20	CTG Leu	GGC Gly	GCC Ala	TGG Trp	GGC Gly 25	CAC His	CCC Pro	GCC/ Al/a	TTC Phe	CCC Pro 30	97
TCC TGC Ser Cys	GGG Gly	CGC Arg	CTC Leu 35	AAG Lys	GAG Glu	GAC Asp	AGC Ser	AGG Arg 40	TAC Tyr	ATC Ile	TTC/ Phe	TTC Phe	ATG Met 45	GAG Glu	145
CCC GAG Pro Glu	GCC Ala	AAC Asn 50	AGC Ser	AGC Ser	GGC Gly	GGG Gly	CCC Pro 55	GGC Gly	CGC Arg	CTT Len	CCG Pro	AGC Ser 60	CTC Leu	CTT Leu	193
CCC CCC Pro Pro	TCT Ser 65	CGA Arg	GAC Asp	GGG Gly	CCG Pro	GAA Glu 70	CCT Pro	CAA Gln	GAA Glu	GGA Gly	GGT Gly 75	CAG Gln	CCG Pro	GGT Gly	241
GCT GTG Ala Val 80															289
CAG GAG Gln Glu 95	TCT Ser	GTG Val	GCA Ala	GGT Gly 100	TCC Ser	AAA Lys	CTA Leu	OTG Val	CTT Leu 105	CGG Arg	TGC Cys	GAG Glu	ACC Thr	AGT Ser 110	337
TCT GAA Ser Glu	TAC Tyr	TCC Ser	TCT Ser 115	CTC Leu	AAG Lys	TTC Phe	AAG Lys	TGG Trp 120	TTC Phe	AAG Lys	AAT Asn	GGG Gly	AGT Ser 125	GAA Glu	385
TTA AGC Leu Ser															433
GGG AAG Gly Lys	TCA Ser 145	GAA Glu	CTT Leu	CGC Arg	ATT Ile	AGC Ser 150	AAA Lys	GCG Ala	TCA Ser	CTG Leu	GCT Ala 155	GAT Asp	TCT Ser	GGA Gly	481
GAA TAT Glu Tyr 160	Met	Cys		Va1		Ser	Lys	Leu	Gly	Asn	Asp				529
GCC AAC Ala Asn 175	ATC Ile	ACC Thr	ATT Ile	GTG Val 180	GAG Glu	TCA Ser	AAC Asn	GCC Ala	ACA Thr 185	TCC Ser	ACA Thr	TCT Ser	ACA Thr	GCT Ala 190	577
GGG ACA Gly Thr															625
GTG AAT Val Asn															673
AGA TAG Arg Tyr															721
AAC TAC Asn Tyr															769

CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAG 827 Leu Pro Glu 255

ATTCCGCCTA GAGCTAGATG CGTTTTACCA GGTCTAACAT TGACTGCCTC TGCCTGTCGC ATGAGAACAT TAACACAAGC GATTGTATGA CTTCCTCTGT CCGTGACTAG TÆGGCTCTGA GCTACTCGTA GGTGCGTAAG GCTCCAGTGT TTCTGAAATT GATCTTGAAT /TACTGTGATA 1007 CGACATGATA GTCCCTCTCA CCCAGTGCAA TGACAATAAA GGCCTTGAAX AGTCAAAAAA 1067 AAAAAAAAA AAAAATCGA TGTCGACTCG AGATGTGGCT G 1108

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:

245

- (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH:

(B) TYPE:

nucleic acid

(C) STRANDEDNESS: (D) TOPOLOGY:

single linear

- (ix) FEATURE:
 - OTHER INFORMATION: N in position 214 is unknown.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC 60 GGCGGCTGCC CAGGCGATGC GAGCGCGGGC/CGGACGGTAA TCGCCTCTCC CTCCTCGGGC 120 TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180 CCAGCGGCGC GCCAGCAGGA GCCACCCÓGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC 240 AGTCCCAGGT GGCCCGGACC GCACG/TGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC 300 GCTCCCCCC ACGCCGCGC CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC 360 AAACTTTTCC CGAAGCCGAT CÉCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC 420 CGGGAGCCGT CCGCGCAGAG/CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA 474 Met Ser Glu Arg Arg

GAA GGC AAA GGC AXG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG 522 Glu Gly Lys Gly Lys Gly Lys Gly Lys Lys Asp Arg Gly Ser Gly

AAG AAG CCC GTØ CCC GCG GCT GGC GGC CCG AGC CCA G 559 Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala /25 3.0

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:
 - SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

252

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

single

(D) TOPOLOGY:

(D) OTHER INFORMATION: N in position 8 could be either A or G.																
	(xi)	SEÇ	QUENC	CE DE	SCRI	PTIC)N: 5	SEQ 1	D NC): 13	17:		/			
CC C	CAT (His (CAN C	GTG 7	rgg o	GCG C Ala A 5	SCG A	AAA (Lys <i>I</i>	GCC (egg (GC T Hy I 10	TTG A Leu I	AAG A	AAG C Ays I	SAC T Asp S	rcg Ser 15	47
CTG Leu	CTC Leu	ACC Thr	GTG Val	CGC Arg 20	CTG Leu	GGC Gly	GCC Ala	TGG Trp	GGC Gly 25	CAC His	CCC Pro	GCC Ala	TTC Phe	CCC Pro 30	TCC Ser	95
TGC Cys	GGG Gly	CGC Arg	CTC Leu 35	AAG Lys	GAG Glu	GAC Asp	AGC Ser	AGG Arg 40	TAC Tyr	ATC Ile/	TTC Phe	TTC Phe	ATG Met 45	GAG Glu	CCC Pro	143
GAG Glu	GCC Ala	AAC Asn 50	AGC Ser	AGC Ser	GGC Gly	GGG Gly	CCC Pro 55	GGC Gly	CGC Arg/	CTT Leu	CCG Pro	AGC Ser 60	CTC Leu	CTT Leu	CCC Pro	191
CCC Pro	TCT Ser 65	CGA Arg	GAC Asp	GGG Gly	CCG Pro	GAA Glu 70	CCT Pro	CAA Gln/	GAA Glu	GGA Gly	GGT Gly 75	CAG Gln	CCG Pro	GGT Gly	GCT Ala	239
		CGG Arg		G												252
							,									
(2)	INFO	ORMA	CION	FOR	SEQU	јеи91	/ E IDI	ENTI	FICAT	CION	NUMI	BER:	:	138:		
(2)		ORMAT SEQU							FICAT	TION	NUMI	BER:		138:		
(2)		SEQUAL (A)	JENCI LEI TYI	E CHA	ARACT	rekis		3: 11 ni s:	78 ucle: ingle inear	ic ad		BER:		138:		
(2)	(i)	SEQUAL (A)	JENCI LEI TYI STI	E CHA NGTH: PE: RANDE	ARACT : EDMES GY:	reris	STICS	5: 11 nu s: 1:	78 icle: ingle inear	ic ad	cid	BER:		138:		
CCT	(i) (xi)	(A) (B) (C) (D)	JENCI LEN TYI STI TOI QUENG	E CHANGTH: PE: RANDE POLOC CE DE	ARACT EDMES ESCRI	TERIS	ON: S	S: nv s: l: SEQ T	78 uclei ingle inear ID NO	ic ace	eid 38:	AGT	CTG	TGG		48
CCT Leu 1	(i) (xi) TGC Pro	SEQUAL (A) (B) (C) (D) SEQUAL (C)	JENCI LEI TYI STI TOI CCC Arg	NGTH: PE: RANDE POLOG GCT Leu TGC	ARACT EDMES ESCRI TGA Lys	FERIS ES: IPTIC AAG Glu GGT	ON: S AGA His GCG	S: nu s: l: SEQ : TGA Lys	78 icleingle ingle inear ID No AGA Ser 10	ic aces Control GTC GTT GTT	eid 38: AGG Glu CTG	AGT Ser	CTG Val	TGG Ala 15 CCT	Gly	48 96
CCT Leu 1 GTT Ser	(i) (xi) TGC Pro CCA Lys	SEQUENCE (A) (B) (C) (D) SEQUENCE (D) SEQUENCE (D) SEQUENCE (D) AAC	JENCI LEI TYI STI TOI CCC Arg TAG Val 20	GCT Leu GGT GGT GGT GGT GGT GGT GGT G	ARACT EDMES ESCRI TGA Lys TTC Arg	SS: IPTIC AAG Glu GGT Cys AGA	ON: S AGA His GCG Glu ATG	S: nu s: l: SEQ I TGA Lys AGA Thr 25	78 iclesingle inear ID NO AGA Ser 10 CCA Ser GTG	ic aces of the second s	eid 88: AGG Glu CTG Glu	AGT Ser AAT Tyr	CTG Val ACT Ser 30	TGG Ala 15 CCT Ser	Gly CTC Leu ACA	
CCT Leu 1 GTT Ser TCA Lys	(i) (xi) TGC Pro CCA Lys AGT Phe	SEQUENCE (A) (B) (C) (D) SEQUENCE CTC Pro AAC Leu TCA Lys	JENCI LEN TYI STI TOI CCC Arg TAG Val 20 AGT Trp	GCT Leu GGT Phe TCA	EDMES GY: TGA Lys TTC Arg TCA Lys	FERIS SS: IPTIC AAG Glu GGT Cys AGA ASN	ON: SAGA His GCG Glu ATG Gly 40	S: In SEQ I TGA Lys AGA Thr 25 GGA Ser	78 iclesingle inear ID NO AGA Ser 10 CCA Ser GTG Glu GGC	GTC GIN GTT Ser AAT Leu CGG	eid 88: AGG Glu CTG Glu TAA Ser	AGT Ser AAT Tyr GCC Arg	CTG Val ACT Ser 30	TGG Ala 15 CCT Ser	Gly CTC Leu ACA	96
CCT Leu 1 GTT Ser TCA Lys	(i) (xi) TGC Pro CCA Lys AGT Phe CAO Gly 50	SEQUE (A) (B) (C) (D) SEQUE Pro AAC Pro AAC Leu TCA Lys 35	JENCI LEN TYI STI TOI CCC Arg TAG Val 20 AGT Trp	GCT Leu GGT Phe	EDMES GY: ESCRI TGA Lys TTC Arg TCA Lys AGA Ile	FERIS SS: IPTIC AAG Glu GGT Cys AGA ASn TAC Gln 55	ON: S AGA His GCG Glu ATG Gly 40 AGA Lys	SEQ TGA Lys AGA Thr 25 GGA Ser AAA Arg	78 iclesingle inear ID NO AGA Ser 10 CCA Ser GTG Glu GGC Pro	GTC GIn GTT Ser AAT Leu CGG Gly	aid 38: AGG Glu CTG Glu TAA Ser	AGT Ser AAT Tyr GCC Arg 45	CTG Val ACT Ser 30 GAA Lys	TGG Ala 15 CCT Ser	Gly CTC Leu ACA	96 144

(ix) FEATURE:

(A) LENGTH: 122 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:	
G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly 1 5 10 15	46
GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser 20 25 30	94
GCC AAC ATC ACC ATT GTG GAG TCA AAC G Ala Asn Ile Thr Ile Val Glu Ser Asn Ala 35	122
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 140:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 417 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:	
TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC	60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG Lys Ser Glu Leu Arg Ile Ser Lys Ala 1 5	110
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu 10 20 25	158
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly 35 40	206
AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC Lys Arg Cys Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile	254
AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG Lys Val Cys Gly His Thr	302
TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT	362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT	417
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 141:	

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 102 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:	
AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser 1 5 10 15	47
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr 20 25 30	95
TCT TCA T Ser Ser Ser 35	102
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 69 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:	
AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro 1 5 10 15	48
ATG AAA GTC CAA ACC CAA GAA Met Lys Val Gln Thr Gln Glu 20	69
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60	
(AY LENGTH: 60 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xx) SEQUENCE DESCRIPTION: SEQ ID NO: 143:	
AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met	48
CCC AGC TTC TAC Ala Ser Phe Tyr	60

(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 36 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:	
AGT Ser 1	ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu 5	36
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 27 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:	
AAG Lys 1	CAT CTT GGG ATT GAA TTT ATG GAG His Leu Gly Ile Glu Phe Met Glu 5	27
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 569 (B) TYPE: nucleic acid (C) STRANDEDWESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:	
AAA Lys 1	GCG GAG GAG OTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile 5 10 15	48
	ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Tyr Cys 20 25 30	96
	ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser 35 40 45	144
	CGC TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His 50 55 60	192
	1	

CAC His 65	CCC Pro	AAT Asn	CCG Pro	CCC Pro	CCC Pro 70	GAG Glu	AAC Asn	GTG Val	CAG Gln	CTG Leu 75	GTG Val	AAT Asn	CAA Gln	TAC Tyr	GTA Val/ 80	240
TCT Ser	AAA Lys	AAT Asn	GTC Val	ATC Ile 85	TCT Ser	AGC Ser	GAG Glu	CAT His	ATT Ile 90	GTT Val	GAG Glu	AGA Arg	GAG Glu	GCG Ala 95	GAG Glu	288
AGC Ser	TCT Ser	TTT Phe	TCC Ser 100	ACC Thr	AGT Ser	CAC His	TAC Tyr	ACT Thr 105	TCG Ser	ACA Thr	GCT Ala	CAT His	CAT His/ 110	rcc ser	ACT Thr	336
ACT Thr	GTC Val	ACT Thr 115	CAG Gln	ACT Thr	CCC Pro	AGT Ser	CAC His 120	AGC Ser	TGG Trp	AGC Ser	AAT Asn	GGA Gly 125	CAC His	ACT Thr	GAA Glu	384
AGC Ser	ATC Ile 130	ATT Ile	TCG Ser	GAA Glu	AGC Ser	CAC His 135	TCT Ser	GTC Val	ATC Ile	GTG Val	ATG Met 140	TCA Ser	TCC Ser	GTA Val	GAA Glu	432
AAC Asn 145	AGT Ser	AGG Arg	CAC His	AGC Ser	AGC Ser 150	CCG Pro	ACT Thr	GGG Gly	GGC Gly	CCG Pro 155	AGA Arg	GGA Gly	CGT Arg	CTC Leu	AAT Asn 160	480
GGC Gly	TTG Leu	GGA Gly	GGC Gly	CCT Pro 165	CGT Arg	GAA Glu	TGT Cys	AAC Asn	AGC Sex 1/10	TTC Phe	CTC Leu	AGG Arg	CAT His	GCC Ala 175	AGA Arg	528
GAA Glu	ACC Thr	CCT Pro	GAC Asp 180	TCC Ser	TAC Tyr	CGA Arg	GAC Asp	TCT/ Ser 1/85	CCT Pro	CAT His	AGT Ser	G A	AAG			569
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 147: (i) SEQUENCE CHARACTERISTICS:																
(2)		SEQ	JENCI	E CHA	ARAC'	/	/	S:		rion	NUM	BER:	;	147:		
(2)		SEQUAL (A)	JENCI	E CHA NGTH PE: RANDI	ARAC'	rer <i>i</i> s	/	7: n: s:	30	ic a		BER:	;	147:		
(2)	(i)	SEQUAL (A)	JENCI LEI TYI	E CHA NGTH PE: RANDI POLOG	ARACT : EDNE: GY:	TERIS	/ STIC	7: n: s: 1:	30 ucle: ingle inea:	ic a e r	cid	BER:		147:		
G T	(i) (xi)	SEQUAL (A) (B) (C) (D) SEQUAL (D)	JENCI LEI TYI STI TOI QUENC	E CHANGTH PE: RANDI POLOG CE DI	ARACT EDNES SY: ESCRI	TERIS	/ STIC: ON: :	7: ni s: 1: SEQ	30 ucle: ingle inea: ID NO CT CO	ic ade e r O: 1	cid	CA C	CT G	TA G. al A		46
G TA	(i) (xi) AT Gr yr Va 1 CAC	SEQUENCE (A) (B) (C) (D) SEQUENCE (A) SEQUEN	JENCI LEI TYI STI TOI QUENC	E CHA	ARACT EDNE: ESCRI IG AG t T TCC	SS: IPTIC CC AChr T	ON: S	7: 7: 8: 1: SEQ :	30 ucle: ingle: inea: ID No CT Co la A:	ic ace r O: 1 GT A rg M 10	cid 47: TG TG	CA Coer Po	CT G ro V	TA G. al A	sp 15 CCG	46 94
G TATO	(i) (xi) AT GT yr Va 1 CAC His	SEQUENCE (A) (B) (C) (D) SEQUENCE (A) SEQUEN	JENCI LEI TYI STI TOI QUENC CA GO Er A	E CHANGTH PE: RANDI POLOG CE DA AG AGC Ser 20 ACG	ARACT EDINES ESCR: IG AG et Ti 5 TCC Ser ACG	SS: IPTIC CC AC hr Ti CCC Pro	ON: S CC CC hr P: AAG Lys	S: 7: ni s: 1: SEQ TCA TCA Ser	30 ucledingle inea: ID No CT CC la A CCC Pro 25 CCC	ic ader r O: 1 GT A'rg M 10 CCT Pro	cid 47: TG TG et Se	CA Cer Pose	CT G ro V ATG Met GTC	TA G al A TCC Ser 30 AGT	sp 15 CCG Pro	
G TY TTC Phe CCC Pro	(xi) (xi) AT GT Yr Va 1 CAC His GTG Val	SEQUENCE (A) (B) (C) (D) SEQUENCE (C) SEQUEN	JENCI LEI TYI STI TOI QUENC CA GO ET A Pro AGC Ser 35	MGTH PE: RANDI POLOG CE DI CA A' Ia MG AGC Ser 20 ACG Thr	ARACT EDINES ESCR: TG AG TCC Ser ACG Thr	CCC ACTO Pro	ON: S CC CC hr P: AAG Lys TCC Ser CTG	S: 7: ni s: 1: SEQ TCA TCA Ser ATG Met 40 CTC	30 ucle ingle inea: ID No CT CC la A CCC Pro 25 CCC Pro CTT	ic ade r O: 1 GT A'rg M 10 CCT Pro TCC Ser	cid 47: TG TG et So TCG Ser ATG	CA Coer Possible GAA Glu GCG Ala	CT G ro V ATG Met GTC Val 45 CCA	TA G al A TCC Ser 30 AGT Ser CGG	SP 15 CCG Pro CCC Pro	94

,

AAC Asn 80	CCC Pro	GCG Ala	CAT His	GAG Glu	AGC Ser 85	AAC Asn	AGC Ser	CTG Leu	CCC Pro	CCC Pro 90	AGC Ser	CCC Pro	TTG Leu	AGG Arg	ATA Ile 95	286
GTG Val	GAG Glu	GAT Asp	GAG Glu	GAA Glu 100	TAT Tyr	GAA Glu	ACG Thr	ACC Thr	CAG Gln 105	GAG Glu	TAC Tyr	GAA Glu	CCA Pro	GCA Ala 110	CAA Gln	334
GAG Glu	CCG Pro	GTT Val	AAG Lys 115	AAA Lys	CTC Leu	ACC Thr	AAC Asn	AGC Ser 120	AGC Ser	CGG Arg	CGG Arg	GCC Ala	AAA Lys 125	AGA Arg	ACC Thr	382
AAG Lys	CCC Pro	AAT Asn 130	GGT Gly	CAC His	ATT Ile	GCC Ala	CAC His 135	AGG Arg	TTG Leu	GAA Glu	ATG Met	GAC Asp 140	AAC Asn	AAC Asn	ACA Thr	430
GGC Gly	GCT Ala 145	GAC Asp	AGC Ser	AGT Ser	AAC Asn	TCA Ser 150	GAG Glu	AGC Ser	GAA Glu	ACA Thr	GAG Glu 155	GAT Asp	GAA Glu	AGA Arg	GTA Val	478
GGA Gly 160	GAA Glu	GAT Asp	ACG Thr	CCT Pro	TTC Phe 165	CTG Leu	GCC Ala	ATA Ile	CAG Gln	AAC Asn 170	CCC Pro	CTG Leu	GCA Ala	GCC Ala	AGT Ser 175	526
CTC Leu	GAG Glu	GCG Ala	GCC Ala	CCT Pro 180	GCC Ala	TTC Phe	CGC Arg	CTG Leu	GTC Val 185	GAC Asp	AGC Ser	AGG Arg	ACT Thr	AAC Asn 190	CCA Pro	574
ACA Thr	GGC Gly	GGC Gly	TTC Phe 195	TCT Ser	CCG Pro	CAG Gln	GAA Glu	GAA Glu 200	TTG Leu	CAG Gln	GCC Ala	AGG Arg	CTC Leu 205	TCC Ser	GGT Gly	622
GTA Val	ATC Ile	GCT Ala 210	AAC Asn	CAA Gln	GAC Asp	CCT Pro	ATC 1/1e 215	GCT Ala	GTC Val	TAA	AACC	GAA .	ATAC.	ACCC.	АТ	672
AGA'	TTCA(CCT (GTAA	AACT'	TT A	ттт/г.	ATAT.	A AT	AAAG'	TATT	CCA	CCTT	AAA	TTAA	ACAA	730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: /1652 base pairs
 - (B) TYPE: rucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLEQULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B)/LOCATION: 459...1181
 - (D) OTHER INFORMATION:
- (xi/ SEQUENCE DESCRIPTION: SEQ ID NO:148:

AGTTTCC/CC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC 60 GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC 120 TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180 CCAGCÉGCGC GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGGACGGA GCGCCCGCCA 240 GTCCCAGGTG GCCCGGACCG CACGTTGCGT CCCCGCGCTC CCCGCCGGCG ACAGGAGACG 300 CTCGCCCCA CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA 360 AACTTTCCC GAAGCCGATC CCAGCCCTCG GACCCAAACT TGTCGCGCGT CGCCTTCGCC 420

GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA GAA 476 Met Ser Glu Arg Glu 1 5											
GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG											
AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC CGC 572 Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro Arg 25 30 35											
TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA GTG 620 Leu Lys Glu Met Lys Met Gln Glu Ser Val Ala Gly Ser Lys Leu Val 40 45 50											
CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG TGG 668 Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp 55 60 65 70											
TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC ATC 716 Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys Pro Gln Asn Ile 75 80 85											
AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA GCG 764 Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Lev Arg Ile Ser Lys Ala 90 95 100											
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA 812 Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu 105 110 115											
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GAG 860 Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Glu 120 125 130											
ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT TCA 908 Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser Ser 135 140 145 150											
GAG TCT CCC ATT AGA ATA TCA CTA TCA ACA GAA GGA ACA AAT ACT TCT 956 Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr Ser 155 160 165											
TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT 1004 Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys 170 175 180											
GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG 1052 Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met 185 190 195											
GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA AAT 1100 Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn 200 205 210											
GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC 1148 Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr 215 220 230											
AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG CTCAGTCGGT 1201 Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu 235 240											
GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT GCGTTTTACC 1261											

AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG CGATTGTATG 1321 ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA GGCTCCAGTG 1381 TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC ACCCAGTGCA/1441 ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAT CGTTCCACGG 1501 GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG TTAAGTTGTA 1561 ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT TCTTTCTGAC 1621 АААТАААСАС ААТАААААА ААААААААА А (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: nucleic acid (B) TYPE:(C) STRANDEDNESS: single (D) TOPOLOGY: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149: CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG GAC TCG CTG 48 His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu/Lys Lys Asp Ser Leu 10 CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TGC 96 Leu Thr Val Arg Leu Gly Ala Trp Gly His/Pro Ala Phe Pro Ser Cys GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC ATG GAG CCC GAG 144 Gly Arg Leu Lys Glu Asp Ser Arg Tyr/Ile Phe Phe Met Glu Pro Glu 40 GCC AAC AGC AGC GGC GGG CCC GGC CTT CCG AGC CTC CTT CCC CCC 192 Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro 55 TCT CGA GAC GGG CCG GAA CCT/CAA GAA GGA GGT CAG CCG GGT GCT GTG 240 Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val 70 CAA CGG TGC GCC TTG CCT/CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 288 Gln Arq Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu 90 85 TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 336 Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu 105 100 TAC TCC TCT CTC/AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 384 Tyr Ser Ser Lex Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser 115 120 CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 432 Arg Lys Asr Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys 130 135 TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 480 Ser Glu/Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr 145 150 155 ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 528 Met/Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA 576

Ile	Thr	Ile	Val 180	Glu	Ser	Asn	Ala	Thr 185	Ser	Thr	Ser	Thr	Ala 190	Gly	Thr	
AGC Ser	CAT His	CTT Leu 195	GTC Val	AAG Lys	TGT Cys	GCA Ala	GAG Glu 200	AAG Lys	GAG Glu	AAA Lys	ACT Thr	TTC Phe 205	TGT Cys	GTG' Va'l	AAT Asn	624
GGA Gly	GGC Gly 210	GAG Glu	TGC Cys	TTC Phe	ATG Met	GTG Val 215	AAA Lys	GAC Asp	CTT Leu	TCA Ser	AAT Asn 220	CCC Pro	тса Ser	AGA Arg	TAC Tyr	672
TTG Leu 225	TGC Cys	AAG Lys	TGC Cys	CAA Gln	CCT Pro 230	GGA Gly	TTC Phe	ACT Thr	GGA Gly	GCG Ala 235	AGA Arg	TCT Cys	ACT Thr	GAG Glu	AAT Asn 240	720
GTG Val	CCC Pro	ATG Met	AAA Lys	GTC Val 245	CAA Gln	ACC Thr	CAA Gln	GAA Glu	AAG Lys 250	TGC Cys	cca pro	AAT Asn	GAG Glu	TTT Phe 255	ACT Thr	768
GGT Gly	GAT Asp	CGC Arg	TGC Cys 260	CAA Gln	AAC Asn	TAC Tyr	GTA Val	ATG Met 265	Ala	AGC Ser	TTC Phe	TAC Tyr	AGT Ser 270	ACG Thr	TCC Ser	816
ACT Thr	CCC Pro	TTT Phe 275	CTG Leu	TCT Ser	CTG Leu	CCT Pro	GAA Glu 280	TAG	CCCA'	TCT (CAGT	CGGT	GC C	GCTT	TCTT	G 870
TTG	CCGC	ATC '	TCCC	CTCA	GA T'	rccn	CCTA	g Æ	CTAG	ATGC	GTT	TTAC	CAG	GTCT	AACA'	TT 930
GAC	TGCC'	rct (GCCT	GTCG	CA T	GAGA	ACAT/	T AA	CACA	AGCG	ATT	GTAT	GAC '	TTCC	TCTG	TC 990
							/									TG 1050
							/									AG 1110
	TTGA.					/	,									1140
(2)	INF	ORMA	TION	FOR	SEO	ÚENC:	E ID	ENTI	FICA	TION	NUM	BER:		150:		
	(i)	SEQ	UENC	E CH	ARAC	TERI	STIC	S:								
		(B) LE) TY) ST	PE:/	,	ss:		n	764 ucle ingl		cid					
		(D) Т9	POLO	GY:			1	inea	r						
	(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0: 1	50:					
G A	AG T ys S 1	CA G er G	/ AA C lu L	TT C eu A	GC A rg I 5	TT A le S	GC A er L	AA G ys A	la S	CA C er L 10	TG G eu A	CT G la A	AT T sp S	CT G er G	GA G ly G 15	AA 49 lu
TAT Tyr	ATG Met	/ TGC Cys	AAA Lys 20	GTG Val	ATC Ile	AGC Ser	AAA Lys	CTA Leu 25	GGA Gly	AAT Asn	GAC Asp	AGT Ser	GCC Ala 30	TCT Ser	GCC Ala	97
	ATC															
ACA	AGC	CAT	CTT	' GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	193

														,	/		
Thr	Ser 50	His	Leu	Val	Lys	Cys 55	Ala	Glu	Lys	Glu	Lys 60	Thr	Phe	Cya	Val		
AAT Asn 65	GGA Gly	GGC Gly	GAC Asp	TGC Cys	TTC Phe 70	ATG Met	GTG Val	AAA Lys	GAC Asp	CTT Leu 75	TCA Ser	AAT Asn	CCC Pro	TCA Ser	AGA Arg 80	241	
TAC Tyr	TTG Leu	TGC Cys	AAG Lys	TGC Cys 85	CAA Gln	CCT Pro	GGA Gly	TTC Phe	ACT Thr 90	GGA Gly	GCG Ala	AGA Arg/	rGT Cys	ACT Thr 95	GAG Glu	289	·
AAT Asn	GTG Val	CCC Pro	ATG Met 100	AAA Lys	GTC Val	CAA Gln	Thr	CAA Gln 105	GAA Glu	AAA Lys	GCG Ala	/GLu	GAG Glu 110	CTC Leu	TAC Tyr	337	
CAG Gln	AAG Lys	AGA Arg 115	GTG Val	CTC Leu	ACC Thr	ATT Ile	ACC Thr 120	GGC Gly	ATT Ile	TGC Cys	ATC Ile	GCG Ala 125	CTG Leu	CTC Leu	GTG Val	385	
GTT Val	GGC Gly 130	ATC Ile	ATG Met	TGT Cys	GTG Val	GTG Val 135	GTC · Val	TAC Tyr	TGC Cys	AAA Lys	ACC Thr 140	AAG Lys	AAA Lys	CAA Gln	CGG Arg	433	
AAA Lys 145	AAG Lys	CTT Leu	CAT His	GAC Asp	CGG Arg 150	CTT Leu	CGG Arg	CAG Gln	AGC Ser	CTT Leu 155	CGG Arg	TCT Ser	GAA Glu	AGA Arg	AAC Asn 160	481	-
ACC Thr	ATG Met	ATG Met	AAC Asn	GTA Val 165	GCC Ala	AAC Asn	GGG Gly	CCC Pro	CAC His 170	CAC His	CCC Pro	AAT Asn	CCG Pro	CCC Pro 175	CCC Pro	529)
GAG Glu	AAC Asn	GTG Val	CAG Gln 180	CTG Leu	GTG Val	AAT Asn	CAA Oʻln	TAC Tyr 185	GTA Val	TCT Ser	AAA Lys	AAT Asn	GTC Val 190	ATC Ile	TCT Ser	577	j
AGC Ser	GAG Glu	CAT His 195	Ile	GTT Val	GAG Glu	AGA Arg	GAG Glu 200	GCG Ala	GAG Glu	AGC Ser	TCT Ser	TTT Phe 205	TCC Ser	ACC Thr	AGT Ser	625	5
		Thr													CCC Pro	673	3
AGT Ser 225	CAC His	AGC Ser	TGG Trp	AGC Ser	AAT Asn 230	Gly	CAC His	ACT Thr	GAA Glu	AGC Ser 235	ATC Ile	ATT Ile	TCG Ser	GAA Glu	AGC Ser 240	721	L
															AGC Ser	769	
															CGT Arg	817	7
		,	Ser												TAC Tyr	865	5
		Ser					Arg								AGG Arg	913	3
AGA	/ _{AAC}	AAG	GCC	CAC	AGA	TCC	AAA	TGC	ATG	CAG	ATC	CAG	CTT	TCC	GCA	96:	ı

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	Arg 305	Asn	Lys	Ala	His	Arg 310	Ser	Lys	Cys	Met	Gln 315	Ile	Gln	Leu	Ser	Alá 320	
	ACT Thr	CAT His	CTT Leu	AGA Arg	GCT Ala 325	TCT Ser	TCC Ser	ATT Ile	CCC Pro	CAT His 330	TGG Trp	GCT Ala	TCA Ser	TTC Phe	TCT Ser 335	AAG Lys	1009
	ACC Thr	CCT Pro	TGG Trp	CCT Pro 340	TTA Leu	GGA Gly	AGG Arg	TAT Tyr	GTA Val 345	TCA Ser	GCA Ala	ATG Met	ACC Thr	ACC Thr 350	CCG Pro	GCT Ala	1057
	CGT Arg	ATG Met	TCA Ser 355	CCT Pro	GTA Val	GAT Asp	TTC Phe	CAC His 360	ACG Thr	CCA Pro	AGC Ser	TCC Ser	Pro 365	AAG Lys	TCA Ser	CCC Pro	1105
	CCT Pro	TCG Ser 370	GAA Glu	ATG Met	TCC Ser	CCG Pro	CCC Pro 375	GTG Val	TCC Ser	AGC Ser	ACG Thr	ACG Thr 380	GTC Val	TCC Ser	ATG Met	CCC Pro	1153
	TCC Ser 385	ATG Met	GCG Ala	GTC Val	AGT Ser	CCC Pro 390	TTC Phe	GTG Val	GAA Glu	GAG Gla	GAG Glu 395	AGA Arg	CCC Pro	CTG Leu	CTC Leu	CTT Leu 400	1201
	GTG Val	ACG Thr	CCA Pro	CCA Pro	CGG Arg 405	CTG Leu	CGG Arg	GAG Glu	AAG Lys	TAT Tyr 410	GAC Asp	CAC His	CAC His	GCC Ala	CAG Gln 415	CAA Gln	1249
	TTC Phe	AAC Asn	TCG Ser	TTC Phe 420	CAC His	TGC Cys	AAC Asn	CCC/ Pro	GCG Ala 425	CAT His	GAG Glu	AGC Ser	AAC Asn	AGC Ser 430	CTG Leu	CCC Pro	1297
	CCC Pro	AGC Ser	CCC Pro 435	TTG Leu	AGG Arg	ATA Ile	GTO Va/l	GAG Glu 440	GAT Asp	GAG Glu	GAA Glu	TAT Tyr	GAA Glu 445	ACG Thr	ACC Thr	CAG Gln	1345
	GAG Glu	TAC Tyr 450	GAA Glu	CCA Pro	GCT Ala	CAX GYn	GAG Glu 455	CCG Pro	GTT Val	AAG Lys	AAA Lys	CTC Leu 460	ACC Thr	AAC Asn	AGC Ser	AGC Ser	1393
	CGG Arg 465	CGG Arg	GCC Ala	AAA Lys	AGA Azg	ACC Thr 470	AAG Lys	CCC Pro	AAT Asn	GGT Gly	CAC His 475	ATT Ile	GCC Ala	CAC His	AGG Arg	TTG Leu 480	1441
															AGC Ser 495		1489
					Arg					Thr					ATA Ile		1537
															CTG Leu		1585
			Arg												GAA Glu		1633
/		Ala										Asp			GCT Ala		1681
	TAA	AACC	GAA	ATAC	ACCC	AT A	GATT	CACC	T GT	AAAA	CTTT	ATT	TTAT	ATA	ATAA	AGTATT	1741

CCACCTTAAA TTAAACAAAA AAA (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: amino acid (B) TYPE: (C) STRANDEDNESS: linear (D) TOPOLOGY: ` (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151: Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys 10 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys 20 Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln/Asn Tyr Val Met Ala Ser 40 Phe Tyr 50 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acid (B) TYPE: (C) STRANDEDNESS (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152: Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys 20 Gln Pro Gly Phe/Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys Val Gln 50 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 amino acid (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

T/r Val Lys Glu Leu Arg Ala Pro Ser Cys Lys Cys Gln Gln Glu Tyr

 $\operatorname{Gl}\psi$ Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys

Phe Gly Glu Arg Cys Gly Glu Lys Ser Asn Lys Thr His Ser 35 40 45

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

198

(B) TYPE:(C) STRANDEDNESS:

nucleic acid

(D) TOPOLOGY:

single linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 1 5 10

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25/ 30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
35 40 45

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT 192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
50 60

GAA TAG

198

Glu 65

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

192

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

singre

(D) TØPOLOGY:

linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:
- AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 1 5 10 15

GGA GGC/GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
35
40
45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA 192 Yal Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr

156:

55 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: (B) TYPE:

183 nucleic acid

(C) STRANDEDNESS (D) TOPOLOGY:

single linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys AlaackslashGlu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Gly Cys Phe Met Val Tys Asp Leu Ser Asn Pro Ser Arg Tyr 25 2.0

TTG TGC AAG TGC CCA AAT GAG TYT ACT GGT GAT CGC TGC CAA AAC TAC 144 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr 40 35

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr 55

157:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

210

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

single

(D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO ₹ 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser\Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr 40

GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA 192 Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys 55 60

GCG GAG GAG CTC TAC TAA Ala Glu Glu Leu Tyr

210

(i) SEQUENCE CHARACTERISTICS: 267 (A) LENGTH nucleic acid (B) TYPE: (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158: AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144 Leu Cys Lys Cys Gln Pro Gl\/y Phe Thr Gly Ala Arg Cys Thr Glu Asn 40 GTG CCC ATG AAA GTC CAA ACC\CAA GAA AAG TGC CCA AAT GAG TTT ACT 192 Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr 55 GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC 240 Gly Asp Arg Cys Gln Asn Tyr Vall Met Ala Ser Phe Tyr Ser Thr Ser ACT CCC TTT CTG TCT CTG CCT GAA\TAG 267 Thr Pro Phe Leu Ser Leu Pro Glu 85 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: lidear (xi) SEQUENCE DESCRIPTION: SEQ ID \NO: 159: AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96 Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr 20 25 30 TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144 Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGQ CCA AAT GAG TTT ACT 192

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:

Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr 50 60
GGT GAT CGC TGC CAA AAC TAC GTA ATG CCC AGC TTC TAC AAA GCG GAG 240 Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu 65 70 80
GAG CTC TAC TAA Glu Leu Tyr
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:
CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala 1 5 10 15
GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG 95 Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val 20 30
AAA GAC CTT TCA AAT CCC TCA AGA TAC Leu Lys Asp Leu Ser Asn Pro Ser Arg Tyr 35 128
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser 1 5 10 15
AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC 94 Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser 20 25 30
ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg 35 40 45
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:
(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH:
                                 24
         (B) TYPE:
                                 amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY:
                                 /linear
    (ix) FEATURE:
         (D) OTHER INFORMATION: / Xaa in positions 15 and 22 is
unknown.
    (xi) SEQUENCE DESCRIPTION: $EQ ID NO: 162:
Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
                                     10
Met Val Lys Asp Leu Xaa Asn P#o
            20
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:
                                                       163:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH:
                                  nucleic acid
         (B) TYPE:
         (C) STRANDEDNESS
                                  single
         (D) TOPOLOGY:
                                  linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:
ATG AGA TGG CGA CGC GCC CGC CGC TCC GGG CGT CCC GGC CCC CGG 48
Met Arg Trp Arg Arg Ala/Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
GCC CAG CGC CCC GGC TCQ GCC CGC TCG TCG CCG CCG CTG CCG CTG 96
Ala Gln Arg Pro Gly Set Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
CTG CCA CTA CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG 144
Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG 192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
TCC CCG CCC AGC GTG/GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG 240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA 288
Val Val Ile Glu GAy Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
CTC GAC AGG AAG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC 336
Leu Asp Arg Lys/Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
            100/
                               105
GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC 384
Gly Asp Arg G/u Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
        115
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GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC 432 Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro 135 ACC GCC CCG GTG CCC AGC GCC GGC GAG GAG GAG GCG CCC TAT 480 Thr Ala Pro Val Pro Ser Ala Gly Glu\Pro Gly Glu Glu Ala Pro Tyr 155 150 CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG 528 Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC 576 Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala 185 TTC CCC TCC TGC GGG AGG CTC AAG GAG GAQ AGC AGG TAC ATC TTC TTC 624 Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe 200 195 Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg 215 220 210 GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC 720 Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Ash Leu Lys Lys Glu Val 235 230 225 745 AGC CGG GTG CTG TGC AAG CGG TGC G Ser Arg Val Leu Cys Lys Arg Cys 245 (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: (i) SEQUENCE CHARACTERISTICS: 12 (A) LENGTH: amino acid (B) TYPE: (C) STRANDEDNESS: linear (D) TOPOLOGY: (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is unknown. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164: Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ix) FEATURE: (D) OTHER INFORMATION: Xaa in position 1 is unknown.

$m{j}$
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:
Xaa Leu Val Leu Arg
1 5
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
(ix) FEATURE:
(D) OTHER INFORMATION: X a in positions 1, 2, and 3 is unknown.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:
Xaa Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn 1 10
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 60 nucleic acid single linear
(ix) FEATURE:
(D) OTHER INFORMATION: N in positions 25 and 36 is unknown.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:
ATAGGGAAGG GCGGGGGAAG GGCCCCCC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT 60
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ix) FEATURE
(D) OTHER INFORMATION: N in position 16 is unknown.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:
TTTACACATA TATTCNCC 18
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

21

(B) TYPE:

- amino aç⁄id
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:
- Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val

Ile Gly Ala Tyr Thr 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:

422

(B) TYPE:

- amino acid
- (C) STRANDEDNESS:
 (D) TOPOLOGY:
- linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:
- Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg

 1 10 15
- Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu 20 25 30
- Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala 35 40 45
- Ala Ala Gly Asn Gly Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
 50 55 60
- Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala 65 70 75 80
- Val Val Ile Gly Cly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala 85 90 95
- Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
 100 105 110
- Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro 1/5 120 125
- Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
- Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
 145 150 155 160
- Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
- Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala 180 185 190
- The Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe 195 200 205

Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala/Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val 235 Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Gln Leu Lys Glu 250 Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys/Leu Val Leu Arg Cys 265 Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn 280 Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro/Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Lie Asn Lys Ala Ser Leu Ala 315 Asp Ser Gly Glu Tyr Met Cys Lys Val/Ile Ser Lys Leu Gly Asn Asp 330 Ser Ala Ser Ala Asn Ile Thr Ile Vall Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Nal Lys Cys Ala Glu Lys Glu Lys 360 Thr Phe Cys Val Asn Gly Gly Glp Cys Phe Met Val Lys Asp Leu Ser 375 Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp 395 390 385 Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro 410 405 Phe Leu Ser Leu Pro Glu 420

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 171:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:/

69

(B) TYPE:

- amino acid
- (C) STRANDEDNESS:
- (D) TOPOLØGY:

linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:
- Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys 1 10 15
- Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
- Pro Arg Glu Tle Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
- Val Ser Seft Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala

60

50

Asn Thr Ser Ser Ser 65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

19

(B) TYPE:

(C) STRANDEDNESS:

amino aci¢

(D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO/ 172:

Arg Lys Gly Asp Val Pro Gly Pro Arg Val/Lys Ser Ser Arg Ser Thr 1 5 15

Thr Thr Ala

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

231

(B) TYPE:

nucleic acid

(C) STRANDEDNESS:

single linear

(D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION / SEQ ID NO: 173:

CGCGAGCGCC TCAGCGCGC CGCTCGCTCT CCCCCTCGAG GGACAAACTT TTCCCAAACC 60
CGATCCGAGC CCTTGGACCA AACTGGCCTG CGCCGAGAGC CGTCCGCGTA GAGCGCTCCG 120
TCTCCGGCGA GATGTCCGAG CGCAAAGAAG GCAGAGGCAA AGGAAAGAAGG AAGAAGAAGG 180
AGCGAGGCTC CGGCAAGAAG CCGGAGTCCG CGGCGGCAG CCAGAGCCCA G 231

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGT/H:

178

(B) TYPE/

nucleic acid

(C) STRANDEDNESS:

single

(D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC CGGATTGAAA GAGATGAAAA GCCAGGAATC GGCTGCAGGT TCCAAACTAG 60
TCCTTCGGTG TGAAACCAGT TCTGAATACT CCTCTCTCAG ATTCAAGTGG TTCAAGAATG 120
GGAATGAATT GAATCGAAAA AACAAACCAC AAAATATCAA GATACAAAAA AAGCCAGG 178

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:

(i) SEQUENCE CHARACTERISTICS:

									,			
			(B) (C)	LENGTH: TYPE: STRANDI TOPOLO	EDNESS:		122 nucleic single linear	aci	id			
		(xi)	SEQU	JENCE DI	ESCRIPT	ION: SE	Q ID NO:	175	5 : /			
	GAAG	TCAG	AA C	TTCGCAT"	ГА АСАА	AGCATC	ACTGGCTG	AT :	TCTGGAG	AGT	ATATGTGCAA	60
,	AGTG	ATCAC	C A	AATTAGG	AA ATGA	CAGTGC	CTCTGCCA	AT	ATCACCAT	rcg	TGGAATCAAA	120
	CG											122
	(2)	INFO	RMAT	ION FOR	SEQUEN	CE IDEN	TIFICATI	ON 1	NUMBER:		176:	
		(i) s	SEQU!	ENCE CH	ARACTER	ISTICS:						
			(B) (C)	LENGTH TYPE: STRAND TOPOLO	EDNESS:		nucleic single linear	ac	id			
		(xi)	SEQ	UENCE D	ESCRIPT	CION: SE	ON DIVO:	17	6:			
	AGAT	CATC	AC T	GGTATGC	CA GCCI	CAACTG	AAGGAGCA	ATA	TGTGTCT'	TCA	GAGTCTCCCA	60
	TTAG	AATA	rc A	GTATCCA	CA GAAG	GAGCAA	ATACTTCT	TTC .	AT		:	L02
	(2)	INFO	RMAT	ION FOR	SEQUEN	CE IDEN	TIFICATI	ON	NUMBER:		177:	
		(i) :	SEQU	ENCE CH	ARACTEF	RIST/CS:						
			(B) (C)	LENGTH TYPE: STRAND TOPOLO	EDNESS:		128 nucleic single linear	c ac	id			
		(xi)	SEQ	UENCE D	ESCRIPT	rion: se	EQ ID NO:	: 17	7:			
	CTAC	CATCT	AC A	TCCACCA	CT GGG	ACAAGCC	ATCTTGTA	AAA	ATGTGCG	GAG	AAGGAGAAAA	60
	CTTT	CTGT	GT G	AATGGAG	GG /GAGT	rGCTTCA	TGGTGAAA	AGA	CCTTTCA	AAC	CCCTCGAGAT	120
	ACT	rgtgc										128
	(2)	INFO	RMAT	ION FOR	SEQUE	NCE IDEN	NTIFICATI	ION	NUMBER:		178:	
		(i)	SEQU	ence of	ARACTE	RISTICS	: ·					
			(B)	LENGTH TYPE: STRAND TOPOLO	EDNESS	:	69 nucleid single linear		eid:			
		(xi)	SEQ	UENCE D	ESCRIP	rion: si	EQ ID NO	: 17	8:			
	AAG:	rgcca	ac 9	TGGATTC	AC TGG	AGCAAGA	TGTACTG	AGA	ATGTGCC	CAT	GAAAGTCCAA	60
	AAC	CAAGA	a /									69
	(2)	INFO	RMAT	ION FOR	SEQUE	NCE IDEI	NTIFICATI	ION	NUMBER:		179:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 23 nucleic acid single linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:	
TCGG	GCTCCA TGAAGAAGAT GTA	23
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:	
TCC	ATGAAGA AGATGTACCT GCT	23
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181:	
	(i) SEQUENCE CHARACTERISTICS	
	(A) LENGTH: 22 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:	
ATG:	TACCTGC TGTCCTCCTT GA	22
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY: 22 nucleic acid single linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:	
TTG	AAGAAGG ACTCGCTGCT CA	22
(2)	INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 20 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:	

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Cys Thr Ala Cys Ala Thr Cys Thr Ala Cys Ala Thr Cys Cys Ala Cys Cys Cys Ala Thr Cys Ala Cys Thr Gly Gly Gly Ala Cys Ala Ala Gly 20 Cys Thr Thr Gly Thr Ala Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Ala Ala Cys Thr Thr Thr Cys Thr Gly Thr Gly Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly 70 Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala 90 85 Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys/Ala Ala Ala Cys Cys 110 105 100 Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys 120 Thr Cys Gly Gly Cys Thr Cys Cys Ala Thr Gly Ala Ala Gly Ala 135 130 Ala Gly Ala Thr Gly Thr Ala

- (2) INFORMATION FOR SEQ ID NO:189:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 amino a¢ids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Cys Thr Ala Cys Ala Thr C/s Thr Ala Cys Ala Thr Cys Cys Ala Cys 10 Cys Ala Cys Thr Gly Gly Ala Cys Ala Ala Gly Cys Cys Ala Thr 20 25 Cys Thr Thr Gly Thr Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly 40 Ala Gly Ala Ala Gly G/1y Ala Gly Ala Ala Ala Cys Thr Thr Thr Cys Thr Gly Thr Gly Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly Gly Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala 90 Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys Ala Ala Ala Cys Cys Cys 100 105 110 Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys 120 Ala Ala Gly Thr Gly Cys Cys Cys Ala Ala Ala Thr Gly Ala Gly Thr 135 140 Thr Thr Ala Cy/s Thr Gly Gly Thr Gly Ala Thr Cys Gly Cys Thr Gly 150 Cys Cys Ala Ala Ala Ala Cys Thr Ala Cys Gly Thr Ala Ala Thr Gly 165 170 Gly Cys Cys Ala Gly Cys Thr Thr Cys Thr Ala Cys Thr Cys Cys Ala Thr Gly Ala Ala Gly Ala Ala Gly Ala Thr Gly Thr Ala Cys Cys Thr 195 200 200 205